



# **STIC Search Report**

## **Biotech-Chem Library**

**STIC Database Tracking Number: 107436**

**To: Michael Borin**  
**Location: cm1/12a01/12d01**  
**Art Unit: 1631**  
**Thursday, November 06, 2003**

**Cas Serial Number: 09/960481**

**From: Beverly Shears**  
**Location: Biotech-Chem Library**  
**CM1-1E05**  
**Phone: 308-4994**

**beverly.shears@uspto.gov**

### **Search Notes**

Michael,

Searched Seq. ID 5278 using the oligomer parameters. If you were interested in a size limited search, pls. contact me.

Beverly

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

M nucleic - nucleic search, using sw model

run on: November 6, 2003, 01:51:23 ; Search time 1392 Seconds  
(without alignments)  
7376.664 Million cell updates/sec

Hit: US-09-960-481-5278

Perfect score: 251

Sequence: 1 ggtggcagttgtgtgacaca.....gtaagaaganatcaaccgag 251

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 2888711 seqs, 20454813386 residues

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

GenEmbl:\*

- 1: gb\_ba:\*
- 2: gb\_htg:\*
- 3: gb\_in:\*
- 4: gb\_om:\*
- 5: gb\_ov:\*
- 6: gb\_pat:\*
- 7: gb\_ph:\*
- 8: gb\_pl:\*
- 9: gb\_pr:\*
- 10: gb\_ro:\*
- 11: gb\_sts:\*
- 12: gb\_sy:\*
- 13: gb\_un:\*
- 14: gb\_vi:\*
- 15: em\_ba:\*
- 16: em\_fun:\*
- 17: em\_hum:\*
- 18: em\_in:\*
- 19: em\_mu:\*
- 20: em\_om:\*
- 21: em\_or:\*
- 22: em\_ov:\*
- 23: em\_pat:\*
- 24: em\_ph:\*
- 25: em\_pl:\*
- 26: em\_ro:\*
- 27: em\_sts:\*
- 28: em\_un:\*
- 29: em\_vi:\*
- 30: em\_htg\_hum:\*
- 31: em\_htg\_inv:\*
- 32: em\_htg\_other:\*
- 33: em\_htg\_mus:\*
- 34: em\_htg\_pln:\*
- 35: em\_htg\_rod:\*
- 36: em\_htg\_mam:\*
- 37: em\_htg\_vrt:\*
- 38: em\_sy:\*
- 39: em\_htgo\_hum:\*
- 40: em\_htgo\_mus:\*
- 41: em\_htgo\_other:\*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	52.6	21.0	1117	8	MTN3	Y08726 M.truncatul
2	52.4	20.9	553	8	AF151726	AF151726 Dianthus
3	51.8	20.6	1182	8	AF313914	AF313914 Petunia x
4	51.8	20.6	1205	6	AX006355	AX006355 Sequence
5	46	18.3	1252	8	AY087516	AY087516 Arabidops
6	45.6	18.2	902	8	AY086047	AY086047 Arabidops
7	45	17.9	879	6	AX506568	AX506568 Sequence
8	45	17.9	910	8	AY113934	AY113934 Arabidops
9	45	17.9	1269	8	AY087836	AY087836 Arabidops
10	45	17.9	1291	8	AY045949	AY045949 Arabidops
11	44.4	17.7	870	8	AY078041	AY078041 Arabidops
12	44.4	17.7	901	8	AY096594	AY096594 Arabidops
13	44.4	17.7	1157	8	AF361825	AF361825 Arabidops
14	44.4	17.7	1172	8	AF419559	AF419559 Arabidops
15	44.4	17.7	1176	8	BT000808	BT000808 Arabidops
16	44.4	17.7	1196	8	AY070412	AY070412 Arabidops
17	40.4	16.1	1124	8	AY116672	AY116672 Arabidops
18	39.8	15.9	1221	8	AY084672	AY084672 Arabidops
19	39.6	15.8	889	8	AY059108	AY059108 Arabidops
20	39.6	15.8	1209	8	AF095641	AF095641 Arabidops
21	39.6	15.8	1279	8	AY057575	AY057575 Arabidops
22	38.2	15.2	934	8	AY064674	AY064674 Arabidops
23	38.2	15.2	1250	8	AY054548	AY054548 Arabidops
C 24	37.8	15.1	152177	10	AL672064	AL672064 Mouse DNA
25	37.6	15.0	841	11	BV019724	BV019724 S212P6038
C 26	37.4	14.9	167515	5	AL928980	AL928980 Zebrafish
27	37	14.7	139039	2	AP005322	AP005322 Oryza sat
28	37	14.7	144941	2	AP004837	AP004837 Oryza sat
C 29	36.2	14.4	134167	9	AC064814	AC064814 Homo sapi
30	36.2	14.4	180013	2	AC121079	AC121079 Mus muscu
C 31	36.2	14.4	197096	10	AC104329	AC104329 Mus muscu
C 32	36.2	14.4	231992	2	AC126738	AC126738 Rattus no
33	35.8	14.3	6303	9	HSM803904	AL832595 Homo sapi
34	35.8	14.3	159476	9	AC090149	AC090149 Homo sapi
35	35.8	14.3	159531	9	AC090575	AC090575 Homo sapi
C 36	35.8	14.3	169876	9	AC037450	AC037450 Homo sapi
37	35.8	14.3	178743	2	AC136178	AC136178 Rattus no
38	35.8	14.3	203843	2	AC021991	AC021991 Homo sapi
39	35.6	14.2	103699	9	AC034305	AC034305 Homo sapi
C 40	35.6	14.2	123244	10	BX004791	BX004791 Mouse DNA
41	35.6	14.2	123931	9	AC011404	AC011404 Homo sapi
42	35.6	14.2	147876	2	AC144353	AC144353 Homo sapi
43	35.6	14.2	152303	2	AC143335	AC143335 Homo sapi
44	35.6	14.2	160494	9	AC108080	AC108080 Homo sapi
C 45	35.6	14.2	169770	9	AC027763	AC027763 Homo sapi

ALIGNMENTS

RESULT 1

MTN3

LOCUS

MTN3

1117 bp

mRNA

linear

PLN 01-NOV-1997

DEFINITION

M.truncatula mRNA for MtN3 gene.

ACCESSION

Y08726

VERSION

Y08726.1 GI:1619601

KEYWORDS

MtN3 gene.

SOURCE

Medicago truncatula (barrel medic)

ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; Core eudicots;  
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;  
Medicago.

REFERENCE

1 (bases 1 to 1117)

AUTHORS

Gamas,P., Niebel Fde,C., Lescure,N. and Cullimore,J.



CDS	56. .853	/note="nectary-specific"	
		/codon_start=1	
		/product="NEC1"	
		/protein_id="AAG34696.1"	
		/db_xref="GI:11345413"	
		/translation="MAQLRADDLSEFIFGLLGNIVSFMVFLAPVPTFFYKIYKRKSSEGY	
		QAIPYMVALFSAGLLYYAYLRKNAYLIVSINGFGCAIELTYISLFLYAPRKSXI	
		FTKSGWLMLELALGALGMVPIITYLLAEGSHRVMIVGICAAINAVFAAPLSIMRQV	
		IKTSVEFMPFTLSLFTLCATMWFYGFYFKKDFYIAPFNILGFLGIVQMLLYFVYK	
		DSKRI DDEKSDPVREATKSEGVETIINIEDNSDNALQSMKDFSLRRTSK"	
ASE COUNT	372 a	209 c	220 g
ORIGIN		381 t	
Query Match	20.6%	Score 51.8;	DB 8; Length 1182;
Best Local Similarity	70.8%	Pred. No. 0.00055;	
Matches	68;	Conservative 0;	Mismatches 28; Indels 0; Gaps 0;
y	155	TTTCGCCTTTGGGATTCTAGGTAACATTGCCTCCTTCCTGCTGCTTTCTGGCACCAC	TACC 214
b	85	TTTTATATTGGCCTTCTTGGTAATATTGTATCATTCATTCATGCTTCTCCTAGCAC	CGTGCC 144
y	215	AACATTTTATAGAGTTTGTAAAGANATCAACCGA	250
b	145	AACATTTTACAAAATATATAAAGGAATCATCAGA	180
ESULT 4			
X006355	AX006355	1205 bp	DNA linear PAT 06-SEP-2000
OCUS	Sequence 4	from Patent WO0004176.	
EPINITION	AX006355	CCSESSION	
ERSION	AX006355.1	GI:9994501	
EYWORDS	Petunia x hybrida		
OURCE	Petunia x hybrida		
ORGANISM	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;		
	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;		
	Asteridae; lamids; Solanales; Solanaceae; Petunia.		
EPERENCE	1		
AUTHORS	Angenent,G.C., Creemers,J. and Kater,M.M.		
TITLE	Process to collect metabolites from modified nectar by insects		
JOURNAL	Patent: WO 0004176-A 4 27-JAN-2000;		
	ANGENENT GERRIT CORNELIS (NL); CREEMERS JANTINA (NL); KATER MARTIN		
	MARIA (NL); STICHTING CT VOOR PLANTENVERED (NL)		
EATURES	Location/Qualifiers		
source	1. .1205		
	/organism="Petunia x hybrida"		
	/mol_type="genomic DNA"		
	/strain="W115"		
	/db_xref="taxon:4102"		
	/tissue_type="nectar gland"		
CDS	79. .876		
	/note="NEC1"		
	/codon_start=1		
	/protein_id="CAC07355.1"		
	/db_xref="GI:9994502"		
	/translation="MAQLRADDLSEFIFGLLGNIVSFMVFLAPVPTFFYKIYKRKSSEGY		
	QAIPYMVALFSAGLLYYAYLRKNAYLIVSINGFGCAIELTYISLFLYAPRKSXI		
	FTKSGWLMLELALGALGMVPIITYLLAEGSHRVMIVGICAAINAVFAAPLSIMRQV		
	IKTSVEFMPFTLSLFTLCATMWFYGFYFKKDFYIAPFNILGFLGIVQMLLYFVYK		
	DSKRI DDEKSDPVREATKSEGVETIINIEDNSDNALQSMKDFSLRRTSK"		
ASE COUNT	374 a	219 c	229 g
RIGIN		383 t	
Query Match	20.6%	Score 51.8;	DB 6; Length 1205;
Best Local Similarity	70.8%	Pred. No. 0.00055;	
Matches	68;	Conservative 0;	Mismatches 28; Indels 0; Gaps 0;
y	155	TTTCGCCTTTGGGATTCTAGGTAACATTGCCTCCTTCCTGCTGCTTTCTGGCACCAC	TACC 214
b	108	TTTTATATTGGCCTTCTTGGTAATATTGTATCATTCATTCATGCTTCTCCTAGCAC	CGTGCC 167

QY	215	AACATTTTATAGAGTTTGTAAAGANATCAACCGA	250
Db	168	AACATTTTACAAAATATATAAAGGAATCATCAGA	203
RESULT 5			
AY087516	AY087516	1252 bp	mRNA linear PLN 14-APR-2003
LOCUS	Arabidopsis thaliana clone 36264	mRNA, complete sequence.	
DEFINITION	AY087516		
ACCESSION	AY087516.1	GI:21406253	
VERSION	FLI CDNA.		
KEYWORDS	Arabidopsis thaliana (thale cress)		
SOURCE	Arabidopsis thaliana		
ORGANISM	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;		
	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;		
	rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.		
REFERENCE	1 (bases 1 to 1252)		
AUTHORS	Haas,B.J., Volfovsky,N., Town,C.D., Troukhan,M., Alexandrov,N.,		
	Feldmann,K.A., Flavell,R.B., White,O. and Salzberg,S.L.		
TITLE	Full-length messenger RNA sequences greatly improve genome		
	annotation		
JOURNAL	Genome Biol. 3 (6), RESEARCH0029 (2002)		
MEDLINE	22088475		
PUBMED	12093376		
REFERENCE	2 (bases 1 to 1252)		
AUTHORS	Brover,V., Troukhan,M., Alexandrov,N., Lu,Y.-P., Flavell,R. and		
	Feldmann,K.		
TITLE	Full-length cDNA from Arabidopsis thaliana		
JOURNAL	Unpublished		
REFERENCE	3 (bases 1 to 1252)		
AUTHORS	Brover,V., Troukhan,M., Alexandrov,N., Lu,Y.-P., Flavell,R. and		
	Feldmann,K.		
TITLE	Direct Submission		
JOURNAL	Submitted (11-MAR-2002) Ceres, Inc, 3007 Malibu Canyon Road,		
	Malibu, CA 90265, USA		
COMMENT	This clone sequence is one of 5,000 Ceres full-length cDNAs made		
	available to TIGR and Genbank. The following quality assessment of		
	this set was done by comparison with known proteins: two percent of		
	the clones are estimated to be 5'-truncated; less than one percent		
	are 3'-truncated; approximately two percent represent alternative		
	splice variants, including unspliced introns and spliced exons; one		
	percent may contain premature stop codons; five percent may have		
	frame shifts in a coding region. A sequence is considered to be		
	5'-truncated if it lacks the translation initiation start (ATG). A		
	sequence is considered to be 3'-truncated if it lacks the		
	C-terminal end of the encoded protein. Please note that these cDNA		
	sequences are derived from the Ws or Laer ecotypes and therefore		
	may contain polymorphisms when compared to sequences from Col-0.		
	Genet carried out the library production and sequencing of the		
	full-length clones. Ceres, Inc. carried out the clustering of the		
	5' sequences, selection of clones, and sequence assembly.		
FEATURES	Location/Qualifiers		
source	1. .1252		
	/organism="Arabidopsis thaliana"		
	/mol_type="mRNA"		
	/db_xref="taxon:3702"		
	/clone="36264"		
	165. .1049		
	/codon_start=1		
	/product="MtN3-like protein"		
	/protein_id="AAM65058.1"		
	/db_xref="GI:21593109"		
	/translation="MALTNLWAFVFGILNIIISFVVFLAPVPTFVRICKKSTEGFQ		
	SLPYVSALFSAMLWIYAMQKDGTAFLITINAPGCVIETIYIVLFSYANKKTRIST		
	LKVLGLLNLPLGFAIIVLCZLLTKGSTREKVLGGICVGSVSFAAPLSIMRVVVRTR		
	SVEFMPFSLSLFTISAVTWLIFYGLAIKOFYVALPNVLGAVQVMILYIIPKYKT		
	PVAQKTDKSKOVSDHSIDIAKLTTVIPGAVLDSAVHQPPALHNVPETKIQLTEVKSQN		
	MTDPKQINQVQKQSQV"		
BASE COUNT	335 a	269 c	234 g
ORIGIN		413 t	1 others
Query Match	18.3%	Score 46;	DB 8; Length 1252;





Deng,J.M., Goldsmith,A.D., Lee,J.M., Onodera,C.S., Quach,H.L., Tang,C., Toriumi,M., Wu,H.C., Yamamura,Y., Yu,G., Bowser,L., Carninci,P., Chen,H., Cheuk,R., Hayashizaki,Y., Ishida,J., Jones,T., Kamiya,A., Karlin-Neumann,G., Kawai,J., Kim,C., Lam,B., Lin,J., Miranda,M., Narusaka,M., Nguyen,M., Palm,C.J., Sakurai,T., Satou,M., Seki,M., Shinn,P., Southwick,A., Shinozaki,K., Davis,R.W., Ecker,J.R. and Theologis,A.

Arabidopsis Open Reading Frame (ORF) Clones

Unpublished

2 (bases 1 to 910)

Yamada,K., Banh,J., Chan,M.M., Chang,C.H., Chang,E., Dale,J.M., Deng,J.M., Goldsmith,A.D., Lee,J.M., Onodera,C.S., Quach,H.L., Tang,C.C., Toriumi,M., Wu,H.C., Yamamura,Y., Yu,G., Bowser,L., Carninci,P., Chen,H., Cheuk,R., Hayashizaki,Y., Ishida,J., Jones,T., Kamiya,A., Karlin-Neumann,G., Kawai,J., Kim,C., Lam,B., Lin,J., Miranda,M., Narusaka,M., Nguyen,M., Palm,C.J., Sakurai,T., Satou,M., Seki,M., Shinn,P., Southwick,A., Shinozaki,K., Davis,R.W., Ecker,J.R. and Theologis,A.

Direct Submission

Submitted (16-MAY-2002) Plant Gene Expression Center, 800 Buchanan Street, Albany, CA 94710, USA

The RIKEN Genomic Sciences Center (GSC) members carried out the collection and clustering of RAFL cDNAs (RAFL cDNA : 'RIKEN Arabidopsis Full-Length cDNA'): Seki,M., Narusaka,M., Ishida,J., Satou,M., Kamiya,A., Sakurai,T., Carninci,P., Kawai, J., Hayashizaki,Y. and Shinozaki,K.

The Salk, Stanford, PGEC (SSP) Consortium members constructed and sequenced the PUNI (ORF) clones using the RAFL cDNAs: Yamada,K., Banh,J., Chan,M.M., Chang,C.H., Chang,E., Dale,J.M., Deng,J.M., Goldsmith,A.D., Lee,J.M., Onodera,C.S., Quach,H.L., Tang,C.C., Toriumi,M., Wu,H.C., Yamamura,Y., Yu,G., Bowser,L., Chen,H., Cheuk,R., Jones,T., Karlin-Neumann,G., Kim,C., Lam,B., Lin,J., Miranda,M., Nguyen,M., Palm,C.J., Shinn,P., Southwick,A., Davis,R.W., Ecker,J.R. and Theologis,A.

Yamada,K. (SSP/PGEC) and Seki, M. (RIKEN GSC) contributed equally to this work. Shinozaki,K. (RIKEN GSC) and Theologis,A. (SSP /PGEC) contributed equally to this work as PIs.

Annotation is based on the January 2002 version of the Arabidopsis genome submitted to GenBank.

EATURES

source

Location/Qualifiers

1. .910

/organism="Arabidopsis thaliana"

/mol\_type="mRNA"

/db\_xref="taxon:3702"

/chromosome="5"

/clone="U10278"

/note="This clone is in PUNI 51.

ecotype: Columbia"

1. .910

/gene="At5g13170"

1. .879

/gene="At5g13170"

/note="contains prokaryotic membrane lipoprotein lipid attachment site AA47-57"

/codon\_start=1

/evidence=experimental

/product="putative senescence-associated protein SAG29"

/protein\_id="AA4982.1"

/db\_xref="GI:21281010"

/translation="MGVMIHHFLAFIFGILGNVISFLVFLAPVTFYRIYKRKSTES FQSLPYQVSLFSCMLWLYALIKDAFLITINSFGCVETLYIAMFFAYATREKRIS AMKLFIAMNVAFFSLIMVTHFWVKTPLQVSLGICVAISVSPAAPLMIVARVIK TKSVEYMPFTLSFFLTISAVMWFAYGLFLNDICIAIPNVGVFLGLQMVLYLVYRNS NEKPEKINSSEQQLKSIVMSPGVSEVHPVVTESVDPPLSEAVHHEDLSKVTKVEEPS IENGKCYVEATRPETV"

880. .910

/gene="At5g13170"

3' UTR

226 a 203 c 201 g 280 t

ASE COUNT

RIGIN

Query Match

Best Local Similarity 17.9%; Score 45; DB 8; Length 910;

Matches 69; Conservative 0; Mismatches 41; Indels 0; Gaps 0;

QY 141 CACAGTCATCTAAGTTTCGCCCTTTGGGATTCTAGGTAACATTGCTCCTCGTGTGCTTT 200

Db 19 CACCATTTCTCGCTTTTATCTTCGGCATCTTAGGAAACGTGATATCCTTCCTGTATTC 78

QY 201 CTGGCACCCTACCAACATTTTATAGAGTTTGTAAAGAAGANATCAACCGA 250

Db 79 CTCGCTCCAGTGCCAACTTTTATAGAATATACAAGAGAGAAAATCGACGGA 128

RESULT 9

AY087836

LOCUS

DEFINITION

Arabidopsis thaliana clone 38843 mRNA, complete sequence.

ACCESSION

AY087836

VERSION

AY087836.1 GI:21406587

KEYWORDS

FLI CDNA.

SOURCE

Arabidopsis thaliana (thale cress)

ORGANISM

Arabidopsis thaliana

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

REFERENCE

1 (bases 1 to 1269)

AUTHORS

Haas,B.J., Volfovsky,N., Town,C.D., Troukhan,M., Alexandrov,N., Feldmann,K.A., Flavell,R.B., White,O. and Salzberg,S.L.

TITLE

Full-length messenger RNA sequences greatly improve genome annotation

JOURNAL

Genome Biol. 3 (6), RESEARCH0029 (2002)

MEDLINE

22088475

PUBMED

12093376

REFERENCE

2 (bases 1 to 1269)

AUTHORS

Brover,V., Troukhan,M., Alexandrov,N., Lu,Y.-P., Flavell,R. and Feldmann,K.

TITLE

Full-Length cDNA from Arabidopsis thaliana

JOURNAL

Unpublished

REFERENCE

3 (bases 1 to 1269)

AUTHORS

Brover,V., Troukhan,M., Alexandrov,N., Lu,Y.-P., Flavell,R. and Feldmann,K.

TITLE

Direct Submission

JOURNAL

Submitted (11-MAR-2002) Ceres, Inc, 3007 Malibu Canyon Road, Malibu, CA 90265, USA

COMMENT

This clone sequence is one of 5,000 Ceres full-length cDNAs made available to TIGR and Genbank. The following quality assessment of this set was done by comparison with known proteins: two percent of the clones are estimated to be 5'-truncated; less than one percent are 3'-truncated; approximately two percent represent alternative splice variants, including unspliced introns and spliced exons; one percent may contain premature stop codons; five percent may have frame shifts in a coding region. A sequence is considered to be 5'-truncated if it lacks the translation initiation start (ATG). A sequence is considered to be 3'-truncated if it lacks the C-terminal end of the encoded protein. Please note that these cDNA sequences are derived from the Ws or LAer ecotypes and therefore may contain polymorphisms when compared to sequences from Col-0. Genset carried out the library production and sequencing of the full-length clones. Ceres, Inc. carried out the clustering of the 5' sequences, selection of clones, and sequence assembly.

FEATURES

source

Location/Qualifiers

1. .1269

/organism="Arabidopsis thaliana"

/mol\_type="mRNA"

/db\_xref="taxon:3702"

/clone="38843"

136. .1014

/codon\_start=1

/product="senescence-associated protein (SAG29)"

/protein\_id="AAM65389.1"

/db\_xref="GI:21593422"

/translation="MGVIINHHPFLAFIFGILGNVISFLVFLAPVTFYRIYKRKSTES FQSLPYQVSLFSCMLWLYALIKDAFLITINSFGCVETLYIAMFFAYATREKRIS

CDS











Kawai,J., Lam,B., Lee,J.M., Lin,J., Liu,S.X., Miranda,M., Narusaka,M., Nguyen,M., Onodera,C.S., Palm,C.J., Pham,P.K., Quach,H.L., Sakurai,T., Satou,M., Seki,M., Southwick,A., Tang,C.C., Toriumi,M., Yamada,K., Yamamura,Y., Yu,G., Yu,S., Shinozaki,K., Davis,R.W., Theologis,A. and Ecker,J.R.

Direct Submission

Submitted (14-SEP-2001) Salk Institute Genomic Analysis Laboratory (SIGNAL), Plant Biology Laboratory, The Salk Institute for Biological Studies, 10010 N. Torrey Pines Road, La Jolla, CA 92037, USA

RIKEN Genomic Sciences Center (GSC) members carried out the collection and clustering of RAFL cDNAs (RAFL cDNA : 'RIKEN Arabidopsis Full-length cDNA') : Seki,M., Narusaka,M., Ishida,J., Satou,M., Kamiya,A., Sakurai,T., Carninci,P., Kawai,J., Hayashizaki,Y. and Shinozaki,K.

The Salk, Stanford, PGECC (SSP) Consortium members carried out the sequencing and annotation of the RAFL cDNAs: Cheuk,R., Chen,H., Kim,C.J., Koesema,E., Meyers,M.C., Shinn,P., Banh,J., Bowser,L., Dale,J.M., Goldsmith,A.D., Jiang,P.X., Jones,T., Karlin-Neumann,G., Lam,B., Lee,J.M., Lin,J., Liu,S.X., Miranda,M., Nguyen,M., Onodera,C.S., Palm,C.J., Pham,P.K., Quach,H.L., Southwick,A., Tang,C.C., Toriumi,M., Yamada,K., Yamamura, Y., Yu,G., Yu,S., Davis,R.W., Theologis,A., and Ecker,J.R.

Cheuk,R. (SSP/Salk) and Seki,M. (RIKEN GSC) contributed equally to this work. Shinozaki,K. (RIKEN GSC) and Ecker,J.R. (SSP/Salk) contributed equally to this work as PIs.

Location/Qualifiers

1. .1172

/organism="Arabidopsis thaliana"

/mol\_type="mRNA"

/db\_xref="taxon:3702"

/chromosome="3"

/clone="RAFL09-07-I01(R14071)"

/note="ecotype: Columbia"

1. .88

89. .958

/note="MTN3-like protein"

/codon\_start=1

/product="AT3g48740/T8P19\_250"

/protein\_id="AAL31891.1"

/db\_xref="GI:16930411"

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959. .1172

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ASE COUNT

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RESULT 15

T000808

OCUS

BT000808

Arabidopsis thaliana At3g48740 mRNA linear PLN 01-OCT-2002

EFINITION

BT000808

CCESION

BT000808.1

ERSION

BT000808.1

GI:23397319

EYWORDS

FLI\_CDNA.

Arabidopsis thaliana (thale cress)

Arabidopsis thaliana

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi.

1 (bases 1 to 1176)

Yamada,K., Chan,M.M., Chang,C.H., Dale,J.M., Hsuan,V.W., Lee,J.M., Quach,H.L., Tang,C., Toriumi,M., Wallender,E.K., Wong,C., Wu,H.C., Yu,G., Yuan,S., Carninci,P., Chen,H., Cheuk,R., Hayashizaki,Y., Ishida,J., Jones,T., Kamiya,A., Kawai,J., Kim,C.J., Narusaka,M., Nguyen,M., Palm,C.J., Sakurai,T., Satou,M., Seki,M., Shinn,P., Southwick,A., Tripp,M.G., Wu,T., Shinozaki,K., Davis,R.W., Ecker,J.R. and Theologis,A.

Arabidopsis Full Length cDNA Clones

Unpublished

2 (bases 1 to 1176)

Yamada,K., Chan,M.M., Chang,C.H., Dale,J.M., Hsuan,V.W., Lee,J.M., Quach,H.L., Tang,C.C., Toriumi,M., Wallender,E.K., Wong,C., Wu,H.C., Yu,G., Yuan,S., Carninci,P., Chen,H., Cheuk,R., Hayashizaki,Y., Ishida,J., Jones,T., Kamiya,A., Kawai,J., Kim,C.J., Narusaka,M., Nguyen,M., Palm,C.J., Sakurai,T., Satou,M., Seki,M., Shinn,P., Southwick,A., Tripp,M.G., Wu,T., Shinozaki,K., Davis,R.W., Ecker,J.R. and Theologis,A.

Direct Submission

Submitted (01-OCT-2002) Plant Gene Expression Center, 800 Buchanan Street, Albany, CA 94710, USA

RIKEN Genomic Sciences Center (GSC) members carried out the collection and clustering of RAFL cDNAs (RAFL cDNA : 'RIKEN Arabidopsis Full-length cDNA') : Seki,M., Narusaka,M., Ishida,J., Satou,M., Kamiya,A., Sakurai,T., Carninci,P., Kawai,J., Hayashizaki,Y. and Shinozaki,K.

The Salk, Stanford, PGECC (SSP) Consortium members carried out the sequencing and annotation of the RAFL cDNAs: Yamada,K., Chan,M.M., Chang,C.H., Dale,J.M., Hsuan,V.W., Lee,J.M., Quach,H.L., Tang,C.C., Toriumi,M., Wallender,E.K., Wong,C., Wu,H.C., Yu,G., Yuan,S., Chen,H., Cheuk,R., Jones,T., Kim,C.J., Nguyen,M., Palm,C.J., Shinn,P., Southwick,A., Tripp,M.G., Wu,T., Davis,R.W., Ecker,J.R. and Theologis,A.

Yamada,K. (SSP/PGECC) and Seki,M. (RIKEN GSC) contributed equally to this work. Shinozaki,K. (RIKEN GSC) and Theologis,A. (SSP/PGECC) contributed equally to this work as PIs.

Annotation based on January 2002 version of the Arabidopsis genome submitted to Genbank.

Location/Qualifiers

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/mol\_type="mRNA"

/db\_xref="taxon:3702"

/chromosome="3"

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ecotype: Columbia"

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91. .960

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/evidence=experimental

934

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/replace="c"

1159

misc\_difference

/gene="At3g48740"

/note="not present in genomic sequence"



GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

DM nucleic - nucleic search, using sw model

Run on: November 5, 2003, 23:11:53 ; Search time 179 Seconds  
(without alignments)  
3785.246 Million cell updates/sec

Title: US-09-960-481-5278  
Perfect score: 251  
Sequence: 1 ggtggcagttgtgtgacaca.....gtaagaaganatcaaccgag 251

Scoring table: IDENTITY\_NUC  
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	54.6	21.8	393	25 ABX22058	Human GDP-mannose
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3	51.8	20.6	847	21 AAZ50207	Clone RC8 for clon
4	51.8	20.6	847	21 AAZ35498	Petunia nectary-sp
5	51.8	20.6	1205	21 AAZ50200	Petunia hybrida ne
6	51.8	20.6	1205	21 AAZ35493	Petunia nectary-sp
7	46.8	18.6	536	25 ABX18522	Human GDP-mannose
8	46	18.3	1252	21 AAC47147	Arabidopsis thalia

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20	42	16.7	1159	21 AAC33952	Arabidopsis thalia
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23	39.8	15.9	1221	21 AAC39463	Arabidopsis thalia
24	38.2	15.2	1219	21 AAC49937	Arabidopsis thalia
25	34.2	13.6	1010	21 AAC48836	Arabidopsis thalia
26	34.2	13.6	1011	21 AAC35497	Arabidopsis thalia
27	34.2	13.6	4188	22 AAF98721	Human late stage o
28	34.2	13.6	4188	25 ABT31937	Human breast cance
C 29	33.6	13.4	89328	24 ABL61995	Colon adenocarcino
C 30	33.4	13.3	5928	22 AAS46766	Tumour suppressor
C 31	33.4	13.3	5928	24 ABL34239	Human immune syste
32	32.8	13.1	2520	23 AAS68697	DNA encoding novel
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C 34	32.8	13.1	2916	24 ABQ91973	Human NF-kB activa
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C 37	32	12.7	3001	21 AAH51715	Chromosome 13q31-q
C 38	31.8	12.7	1893	20 AAV80069	L. helveticus pept
C 39	31.8	12.7	2000	24 ABZ17252	Arabidopsis thalia
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C 42	31.4	12.5	1035	20 AAZ06224	Human secreted pro
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ALIGNMENTS

RESULT 1  
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ID ABX22058 standard; cDNA; 393 BP.  
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AC ABX22058;  
XX  
DT 10-FEB-2003 (first entry)  
XX  
DE Human GDP-mannose 4,6-dehydratase (GM4,6D) DNA #4115.  
XX  
KW Human; GDP-mannose 4,6-dehydratase; GM4,6D; gene; ss; inflammation;  
KW cellular fucosylation; glycoconjugate fucosylation; transplant rejection;  
KW arthritis; asthma; sepsis; reperfusion injury; stroke; infection;  
KW complex carbohydrate; gene replacement therapy; immunosuppressive;  
KW antiinflammatory; antiarthritic; antibacterial; cerebroprotective;  
XX antiasthmatic; vasotropic.  
OS Homo sapiens.  
XX  
PN US2002110548-A1.  
XX  
PD 15-AUG-2002.  
XX

PF 11-JUN-2001; 2001US-0878574.  
XX  
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PR 03-DEC-1997; 97US-0984246.  
PR 09-SEP-1998; 98US-0149674.  
PR 14-JUN-1999; 99US-0333177.  
XX  
PA (GEMY ) GENETICS INST INC.









X S Disclosure; SEQ ID NO 581; 6pp; English.

X C The invention relates to a composition comprising a human GDP-mannose

C 4,6-dehydratase (GM4,6D) peptide. The peptide is useful for identifying

C GM4,6D inhibitors. GM4,6D inhibitors are useful for reducing inflammation

C in a mammalian subject and for treating or ameliorating diseases affected

CC by the level of cellular fucosylation or diseases affected by the

CC fucosylation of glycoconjugates. These diseases include arthritis,

CC transplant rejection, asthma, sepsis, reperfusion injury, stroke or

CC infection. The GM4,6D peptide or a polynucleotide encoding it is also

CC useful for manufacturing complex carbohydrates and as targets for

CC screening small molecule antagonists of the activity of the enzyme. The

CC polynucleotide is useful in developing an assay for defects in the

CC ABX17942-ABX17944 and ABX17947-ABX33716 represent DNA molecules encoding

CC human GM4,6D peptides of the invention.

CC Note: The sequence data for this patent did not form part of the printed

CC specification but was obtained in electronic format directly from USPTO

CC at seqdata.uspto.gov/sequence.html.

IX

Q Sequence 536 BP; 128 A; 123 C; 104 G; 180 T; 1 other;

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Best Local Similarity 61.0%; Pred. No. 0.00012;

Matches 75; Conservative 0; Mismatches 48; Indels 0; Gaps 0;

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130 CTTCGTTGCTTTCTTGGCACCACCTACCAACATTTTATAGAGTTTGTGAAGAAGANATCAAC 247

131 CTTCGAGTGTCTCTGCTCCATTGCCAACCTTTTATCAATCTACAAGAAGAATCCAC 198

248 CGA 250

199 TGA 201

RESULT 8

AAC47147

D AAC47147 standard; DNA; 1252 BP.

X C AAC47147;

X X

T 18-OCT-2000 (first entry)

X E Arabidopsis thaliana DNA fragment SEQ ID NO: 52735.

X X

Hybridisation assay; genetic mapping; gene expression control;

protein identification; signal transduction pathway;

metabolic pathway; promoter; termination sequence; ss.

X X Arabidopsis thaliana.

IX

N EP1033405-A2.

X D

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X X

F 25-FEB-2000; 2000EP-0301439.

X X

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PR 30-APR-1999; 99US-0132048.

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DT 18-OCT-2000 (first entry)

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KW Hybridisation assay; genetic mapping; gene expression control;  
KW protein identification; signal transduction pathway;  
KW metabolic pathway; promoter; termination sequence; ss.

XX

OS Arabidopsis thaliana.

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PN EP1033405-A2.

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PD 06-SEP-2000.

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PR 14-JUN-1999; 99US-0333177.  
XX  
PA (GEMY ) GENETICS INST INC.  
XX  
PI Sullivan F, Kriz R, Kumar R;  
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DR WPI; 2003-066673/06.  
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PS Disclosure; SEQ ID NO 53; 6pp; English.











GenCore version 5.1.6  
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SUMMARIES

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ALIGNMENTS

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; Patent No. 5670367  
; GENERAL INFORMATION:  
; APPLICANT: DORNER, F.  
; APPLICANT: SCHEIFLINGER, F.  
; APPLICANT: FALKNER, F. G.  
; TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS  
; NUMBER OF SEQUENCES: 52  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Polley & Lardner  
; STREET: 1800 Diagonal Road, Suite 500  
; CITY: Alexandria  
; STATE: VA  
; COUNTRY: USA  
; ZIP: 22313-0299  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
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; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/232,463  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/07/935,313  
; FILING DATE:  
; APPLICATION NUMBER: EP 91 114 300.6  
; FILING DATE: 26-AUG-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: BENT, Stephen A.  
; REGISTRATION NUMBER: 29,768  
; REFERENCE/DOCKET NUMBER: 30472/114 IMMU  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (703)836-9300  
; TELEFAX: (703)683-4109  
; TELEX: 899149  
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; CLONE: ptzgt-F1s  
US-08-232-463-14

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APPLICANT: Sun, Dongxu  
TITLE OF INVENTION: METHODS OF SCREENING FOR COMPOUNDS  
TITLE OF INVENTION: ACTIVE ON STAPHYLOCOCCUS AUREUS  
TITLE OF INVENTION: TARGET GENES  
NUMBER OF SEQUENCES: 111  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lyon & Lyon  
STREET: 633 West Fifth Street  
STREET: Suite 4700  
CITY: Los Angeles  
STATE: California  
COUNTRY: U.S.A.  
ZIP: 90071-2066  
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MEDIUM TYPE: storage  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM P.C. DOS 5.0  
SOFTWARE: Word Perfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/265,315  
FILING DATE: March 9, 1999  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
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FILING DATE: September 13, 1996  
APPLICATION NUMBER: 60/009,102  
FILING DATE: December 22, 1995  
APPLICATION NUMBER: 60/003,798  
FILING DATE: September 15, 1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Warburg, Richard J.  
REGISTRATION NUMBER: 32,327  
REFERENCE/DOCKET NUMBER: 240/247  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510  
INFORMATION FOR SEQ ID NO: 88:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 954 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-09-265-315-88

Query Match 12.4%; Score 31.2; DB 3; Length 954;  
Best Local Similarity 41.9%; Pred. No. 1.3;  
Matches 96; Conservative 0; Mismatches 133; Indels 0; Gaps 0;  
QY 3 TGGCAGTGTGTGACACAGAAATTAAGCTAGAGCTTCATAGTTTCTTCTCTCTCAC 62  
Db 107 TGAGAGTCTGCTGAACGTGAATTAATCTATGTTTAAATGAAAATGAAATTAAGCTAT 166  
QY 63 CTTCTCTCTCTCCCTTCAGACAAAGGGACAAAATCNNNNNNNNNNNNNNNNNNN 122  
Db 167 GCTTACCACGTGATGCATGTTATATGAATAAAATATAAACTGTAAACCTTTACGATT 226  
QY 123 NNTTCCAAAACCATGTCCACAGTCATCTAAGTTTCGCCCTTTGGGATTTCTAGGTAACATT 182  
Db 227 ATTTATAAGGTAGAAAGGGTTTGTATGTGGTTAGTCATTATGATTATACATAACAAG 286  
QY 183 GCCTCCTTCGTGCTTTCTGGCACCACCTACCAACATTTTATAGAGTTT 231  
Db 287 GCCCGTTTTTTATGTTGTAGTAAATTAAGTTTGAATAATTTTATAGTTTTT 335

RESULT 7  
US-09-265-315-88  
; Sequence 88, Application US/09265315  
; Patent No. 6187541  
; GENERAL INFORMATION:  
; APPLICANT: Benton, Bret

APPLICANT: Lee, Ving J.  
APPLICANT: Malouin, Francois  
APPLICANT: Martin, Patrick K.  
APPLICANT: Schmid, Molly B.  
APPLICANT: Sun, Dongxu  
TITLE OF INVENTION: METHODS OF SCREENING FOR COMPOUNDS  
TITLE OF INVENTION: ACTIVE ON STAPHYLOCOCCUS AUREUS  
TITLE OF INVENTION: TARGET GENES  
NUMBER OF SEQUENCES: 111  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lyon & Lyon  
STREET: 633 West Fifth Street  
STREET: Suite 4700  
CITY: Los Angeles  
STATE: California  
COUNTRY: U.S.A.  
ZIP: 90071-2066  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
MEDIUM TYPE: storage  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM P.C. DOS 5.0  
SOFTWARE: Word Perfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/265,315  
FILING DATE: March 9, 1999  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/714,918  
FILING DATE: September 13, 1996  
APPLICATION NUMBER: 60/009,102  
FILING DATE: December 22, 1995  
APPLICATION NUMBER: 60/003,798  
FILING DATE: September 15, 1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Warburg, Richard J.  
REGISTRATION NUMBER: 32,327  
REFERENCE/DOCKET NUMBER: 240/247  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510  
INFORMATION FOR SEQ ID NO: 88:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 954 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-09-265-315-88

Query Match 12.4%; Score 31.2; DB 3; Length 954;  
Best Local Similarity 41.9%; Pred. No. 1.3;  
Matches 96; Conservative 0; Mismatches 133; Indels 0; Gaps 0;  
QY 3 TGGCAGTGTGTGACACAGAAATTAAGCTAGAGCTTCATAGTTTCTTCTCTCTCAC 62  
Db 107 TGAGAGTCTGCTGAACGTGAATTAATCTATGTTTAAATGAAAATGAAATTAAGCTAT 166  
QY 63 CTTCTCTCTCTCCCTTCAGACAAAGGGACAAAATCNNNNNNNNNNNNNNNNNNN 122  
Db 167 GCTTACCACGTGATGCATGTTATATGAATAAAATATAAACTGTAAACCTTTACGATT 226  
QY 123 NNTTCCAAAACCATGTCCACAGTCATCTAAGTTTCGCCCTTTGGGATTTCTAGGTAACATT 182  
Db 227 ATTTATAAGGTAGAAAGGGTTTGTATGTGGTTAGTCATTATGATTATACATAACAAG 286  
QY 183 GCCTCCTTCGTGCTTTCTGGCACCACCTACCAACATTTTATAGAGTTT 231  
Db 287 GCCCGTTTTTTATGTTGTAGTAAATTAAGTTTGAATAATTTTATAGTTTTT 335

RESULT 8  
US-09-266-417-88



Sequence 88, Application US/09266417  
Patent No. 6228588

GENERAL INFORMATION:

APPLICANT: Benton, Bret  
APPLICANT: Lee, Ving J.  
APPLICANT: Malouin, Francois  
APPLICANT: Martin, Patrick K.  
APPLICANT: Schmid, Molly B.  
APPLICANT: Sun, Dongxu

TITLE OF INVENTION: METHODS OF SCREENING FOR COMPOUNDS  
TITLE OF INVENTION: ACTIVE ON STAPHYLOCOCCUS AUREUS  
TITLE OF INVENTION: TARGET GENES  
NUMBER OF SEQUENCES: 111  
CORRESPONDENCE ADDRESS: 111

ADDRESSEE: Lyon & Lyon  
STREET: 633 West Fifth Street  
STREET: Suite 4700  
CITY: Los Angeles  
STATE: California  
COUNTRY: U.S.A.  
ZIP: 90071-2066

COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
MEDIUM TYPE: storage  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM P.C. DOS 5.0  
SOFTWARE: Word Perfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/266,417  
FILING DATE: March 9, 1999  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/714,918  
FILING DATE: September 13, 1996  
APPLICATION NUMBER: 60/009,102  
FILING DATE: December 22, 1995  
APPLICATION NUMBER: 60/003,798  
FILING DATE: September 15, 1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Warburg, Richard J.  
REGISTRATION NUMBER: 32,327  
REFERENCE/DOCKET NUMBER: 240/248  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510  
INFORMATION FOR SEQ ID NO: 88:

SEQUENCE CHARACTERISTICS:  
LENGTH: 954 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
S-09-266-417-88

Query Match 12.4%; Score 31.2; DB 3; Length 954;  
Best Local Similarity 41.9%; Pred. No. 1.3;  
Matches 96; Conservative 0; Mismatches 133; Indels 0; Gaps 0;  
y 3 TGGCAGTTGTGTGACACAGAAATTAAGCTAGAGCTTCATAGTTTCTTCTCTTTCTCAC 62  
b 107 TGAGAGTCTGCTGAACGTGAAATTAATCTATGTTTAATGAAATGAAATTAAGTAT 166  
y 63 CTTCTCTCTCTCCCTTCAGACAAAGGGACAAATAATCNNNNNNNNNNNNNNNNNNN 122  
b 167 GCTTCACCACGTGATGTCATGTTATATGAATAAAATATAAACTGTAAACCTTACGATT 226  
y 123 NNTTCCAAACCATGTCCACAGTCATCTAAGTTTCGCCTTTGGGATTTAGGTAACATT 182  
b 227 ATTTATAAAGGTAGAAAGGGTTTGTATGTGGTAGTCATTATGATTATACATAACAAG 286  
y 183 GCCTCCTTCGTGCTTTCTGGCACCACACTACCAACATTTTATAGAGTTT 231  
b 287 GCCCGTTTTTTATGTTGTAGTAAATTAATCTGAAAAATTTTATAGTTTTT 335

RESULT 9

US-07-674-287B-1/c  
; Sequence 1, Application US/07674287B  
; Patent No. 5414076

GENERAL INFORMATION:

APPLICANT: Bryan Mark O'Hara  
TITLE OF INVENTION: Gibbon Ape Leukemia  
TITLE OF INVENTION: Virus Receptor  
NUMBER OF SEQUENCES: 3  
CORRESPONDENCE ADDRESS:

ADDRESSEE: Dr. Karen A. Lowney  
ADDRESSEE: American Cyanamid Company  
STREET: 1937 West Main Street  
STREET: P.O. Box 60  
CITY: Stamford  
STATE: CT  
COUNTRY: USA  
ZIP: 06904-0060

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy Disk  
COMPUTER: IBM PC AT  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: ASCII converted from IBM DW4  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/674,287B  
FILING DATE: 19910325  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Lowney, Karen A., Dr.  
REGISTRATION NUMBER: 31,274  
REFERENCE/DOCKET NUMBER: 31,104-01  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 203 321 2361  
TELEFAX: 203 321 2971  
TELEX: 710 474 4059  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 3211 Base Pairs  
TYPE: NUCLEOTIDE SEQUENCE  
STRANDEDNESS: Single  
TOPOLOGY: Linear  
MOLECULE TYPE: DNA  
US-07-674-287B-1

Query Match 12.4%; Score 31.2; DB 1; Length 3211;  
Best Local Similarity 44.3%; Pred. No. 2;  
Matches 66; Conservative 0; Mismatches 83; Indels 0; Gaps 0;

QY 24 ATTAAGCTAGAGCTTCATAGTTTCTTCTTTCTCACCCTTCCTTCTCCTTCAGAC 83  
Db 1877 ATTCTTCTAGAGAGCCATTACTTCTTTTCTGTCCACCTAGACCCATCGCTGCCTTGACAC 1818  
QY 84 AAAGGGACAAAAAATCNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 143  
Db 1817 TCATGTCTATCTCAGATGCTGAGTGAAGGTCAGACACAGCATTGCAGTAACGTGTTAAAC 1758  
QY 144 AGTCATCTAAGTTTTCGCCCTTTGGGATTCT 172  
Db 1757 TGTCATTGGAATTCGCTTCTTGGAGTCT 1729

RESULT 10

US-08-436-900A-1/c

; Sequence 1, Application US/08436900A  
; Patent No. 5874264  
; GENERAL INFORMATION:  
; APPLICANT: O'Hara, Bryan M.  
; TITLE OF INVENTION: Gibbon Ape Leukemia Virus Receptors









S-08-920-827-3

search completed: November 6, 2003, 03:47:39  
ob time : 54 secs



GenCore version 5.1.6  
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4 nucleic - nucleic search, using sw model

Run on: November 6, 2003, 03:20:38 ; Search time 192 Seconds  
(without alignments)  
4171.512 Million cell updates/sec

Title: US-09-960-481-5278  
Perfect score: 251  
Sequence: 1 ggtggcagtggtgtgacaca.....gtaagaaganatcaaccgag 251

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 2141354 seqs, 1595478879 residues  
Total number of hits satisfying chosen parameters: 4282708

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications NA.\*  
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13: /cgn2\_6/ptodata/2/pubpna/US10A\_PUBCOMB.seq.\*  
14: /cgn2\_6/ptodata/2/pubpna/US10B\_PUBCOMB.seq.\*  
15: /cgn2\_6/ptodata/2/pubpna/US10\_NEW\_PUB.seq.\*  
16: /cgn2\_6/ptodata/2/pubpna/US60\_NEW\_PUB.seq.\*  
17: /cgn2\_6/ptodata/2/pubpna/US60\_PUBCOMB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	54.6	21.8	393	10	US-09-878-574-4117 Sequence 4117, Ap
2	54.6	21.8	394	10	US-09-878-574-4124 Sequence 4124, Ap
3	46.8	18.6	536	10	US-09-878-574-581 Sequence 581, App
4	45.2	18.0	390	10	US-09-878-574-53 Sequence 53, Appl
5	45	17.9	378	10	US-09-878-574-1003 Sequence 1003, Ap
6	45	17.9	389	10	US-09-878-574-257 Sequence 257, App
7	45	17.9	879	10	US-09-938-842A-1263 Sequence 1263, Ap
8	41.4	16.5	438	9	US-09-770-444-965 Sequence 965, App
9	34.2	13.6	4188	14	US-10-176-847-87 Sequence 87, Appl
10	33.8	13.5	612	12	US-10-027-632-94170 Sequence 94170, A
11	33.8	13.5	612	12	US-10-027-632-307887 Sequence 307887, A
12	33.8	13.5	612	13	US-10-027-632-94170 Sequence 94170, A
13	33.8	13.5	612	13	US-10-027-632-307887 Sequence 307887, A
14	33.6	13.4	89328	12	US-09-873-367C-332 Sequence 332, App
15	33.4	13.3	962	12	US-10-027-632-31123 Sequence 31123, A
16	33.4	13.3	962	12	US-10-027-632-31124 Sequence 31124, A

17	33.4	13.3	962	13	US-10-027-632-31123	Sequence 31123, A
18	33.4	13.3	962	13	US-10-027-632-31124	Sequence 31124, A
C 19	33.4	13.3	969	12	US-10-027-632-9097	Sequence 9097, Ap
C 20	33.4	13.3	969	13	US-10-027-632-9097	Sequence 9097, Ap
C 21	33.4	13.3	5928	12	US-10-311-455-2212	Sequence 2212, Ap
22	33.2	13.2	402850	11	US-09-844-653-5	Sequence 5, Appli
23	33	13.1	735	12	US-10-027-632-174320	Sequence 174320,
24	33	13.1	735	12	US-10-027-632-174321	Sequence 174321,
25	33	13.1	735	13	US-10-027-632-174320	Sequence 174320,
26	33	13.1	735	13	US-10-027-632-174321	Sequence 174321,
C 27	32.8	13.1	598	12	US-10-027-632-81002	Sequence 81002, A
C 28	32.8	13.1	598	12	US-10-027-632-301748	Sequence 301748,
C 29	32.8	13.1	598	13	US-10-027-632-81002	Sequence 81002, A
C 30	32.8	13.1	598	13	US-10-027-632-301748	Sequence 301748,
C 31	32.8	13.1	2916	12	US-10-024-298A-124	Sequence 124, App
C 32	32.8	13.1	2916	12	US-10-042-211A-124	Sequence 124, App
C 33	32.8	13.1	3290	10	US-09-981-353-172	Sequence 172, App
C 34	32.8	13.1	3290	11	US-09-919-039-164	Sequence 164, App
C 35	32.8	13.1	3328	12	US-10-240-965-111	Sequence 111, App
C 36	32.4	12.9	810	12	US-10-027-632-29936	Sequence 29936, A
C 37	32.4	12.9	810	12	US-10-027-632-29937	Sequence 29937, A
C 38	32.4	12.9	810	13	US-10-027-632-29936	Sequence 29936, A
C 39	32.4	12.9	810	13	US-10-027-632-29937	Sequence 29937, A
40	32.2	12.8	663	12	US-10-027-632-214541	Sequence 214541,
41	32.2	12.8	663	12	US-10-027-632-214542	Sequence 214542,
42	32.2	12.8	663	12	US-10-027-632-214543	Sequence 214543,
43	32.2	12.8	663	12	US-10-027-632-214544	Sequence 214544,
44	32.2	12.8	663	13	US-10-027-632-214541	Sequence 214541,
45	32.2	12.8	663	13	US-10-027-632-214542	Sequence 214542,

ALIGNMENTS

RESULT 1  
US-09-878-574-4117  
; Sequence 4117, Application US/09878574  
; Patent No. US20020110548A1  
; GENERAL INFORMATION:  
; APPLICANT: Byrum, Joseph R.  
; APPLICANT: La Rosa, Thomas J.  
; APPLICANT: Thompson, Michael D.  
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with  
; TITLE OF INVENTION: Plants  
; FILE REFERENCE: 38-21(15401)B  
; CURRENT APPLICATION NUMBER: US/09/878,574  
; CURRENT FILING DATE: 2001-12-21  
; PRIOR APPLICATION NUMBER: 09/333,535  
; PRIOR FILING DATE: 1999-06-14  
; NUMBER OF SEQ ID NOS: 15775  
; SEQ ID NO 4117  
; LENGTH: 393  
; TYPE: DNA  
; ORGANISM: Glycine max  
; OTHER INFORMATION: Clone ID: LIB3028-001-Q1-B1-C2  
US-09-878-574-4117

Query Match	21.8%	Score	54.6;	DB	10;	Length	393;
Best Local Similarity	66.1%	Pred. No.	1.9e-07;				
Matches	78;	Conservative	0;	Mismatches	40;	Indels	0;
Gaps	0;						
Qy	133	CCATGTCACAGTCATCTAAGTTTCGCCCTTTGGGATTTCTAGGTAACATTCCTCTTCG	192				
Db	71	CAATTTCTGATCATGAACCTGTTTGTATCTTTGGTCTCCTAGGTAACATTTGTGTCAATCA	130				
Qy	193	TGTGCTTTCTGGCACCACTACCAACATTTTATAGAGTTTGTAAAGAGANATCAACCGA	250				
Db	131	TGGTGTCTTAGCACCCCTTGCCCAACCTTCTATACAATTTACAAGAGAAATCATCAGA	188				

RESULT 2  
US-09-878-574-4124  
; Sequence 4124, Application US/09878574











PRIOR FILING DATE: 1999-09-28  
PRIOR APPLICATION NUMBER: US 60/146,002  
PRIOR FILING DATE: 1999-08-09  
NUMBER OF SEQ ID NOS: 325720  
SOFTWARE: FastSEQ for Windows Version 4.0  
SEQ ID NO 31123  
LENGTH: 962  
TYPE: DNA  
ORGANISM: Human  
US-10-027-632-31123

Query Match	13.3%	Score 33.4;	DB 12;	Length 962;
Best Local Similarity	44.9%	Pred. No. 2;		
Matches	70;	Conservative	0;	Mismatches 86; Indels 0; Gaps 0;
yy	12	TGTGACACAGAAATTAAAGCTAGAGCTTCATAGTTTCTTCTTCTTTTCTCACCTTCCTTCT	71	
bb	4	TATGACAGAGATATAAAGAGAAATCCCTCTATTTTCTCTTCTTCTTCTTCTTACGAAGCCCA	63	
yy	72	CTCCCTTCAGACAAAGGGACAAAAAATCNNNNNNNNNNNNNNNNNNNNNNNNNNNNNTTCCAAA	131	
b	64	GTCTATCAGATTAAAGGCCCCACCCCTTATGACTTCAATTTAACCTTAATTACCTCCTGAAG	123	
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bb	124	ACCCTGCTCTGGGATGGTAACGTGGGGTTTAGG	159	

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Job time : 195 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

M nucleic - nucleic search, using sw model

Run on: November 6, 2003, 03:08:28 ; Search time 1394 Seconds  
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4376.201 Million cell updates/sec

Title: US-09-960-481-5278  
Effect score: 251  
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Gapop 10.0 , Gapext 1.0

Searched: 22781392 seqs, 12152238056 residues  
Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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- 1: em\_estba:\*
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  - 3: em\_estin:\*
  - 4: em\_estmu:\*
  - 5: em\_estov:\*
  - 6: em\_estpl:\*
  - 7: em\_estro:\*
  - 8: em\_htc:\*
  - 9: gb\_est1:\*
  - 10: gb\_est2:\*
  - 11: gb\_htc:\*
  - 12: gb\_est3:\*
  - 13: gb\_est4:\*
  - 14: gb\_est5:\*
  - 15: em\_estfun:\*
  - 16: em\_estom:\*
  - 17: em\_gss\_hum:\*
  - 18: em\_gss\_inv:\*
  - 19: em\_gss\_pln:\*
  - 20: em\_gss\_vrt:\*
  - 21: em\_gss\_fun:\*
  - 22: em\_gss\_mam:\*
  - 23: em\_gss\_mus:\*
  - 24: em\_gss\_pro:\*
  - 25: em\_gss\_rod:\*
  - 26: em\_gss\_phg:\*
  - 27: em\_gss\_vrl:\*
  - 28: gb\_gss1:\*
  - 29: gb\_gss2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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3	206	82.1	450	13 BU090931	BU090931 su09e10.y
4	200	79.7	473	10 BE804090	BE804090 sr75f12.y

5	200	79.7	531	12 BM887247	BM887247 sam36a12.
6	200	79.7	580	12 BM520189	BM520189 sak90b05.
7	194	77.3	389	10 BF068522	BF068522 st83b03.y
8	193.6	77.1	457	10 BG041196	BG041196 sv31a02.y
9	192.8	76.8	578	12 BM886347	BM886347 sam15d12.
10	191	76.1	218	13 BU764411	BU764411 sas01a10.
11	191	76.1	593	13 BU764490	BU764490 sas02c05.
12	190.2	75.8	458	13 BU090543	BU090543 su06b06.y
13	189.4	75.5	565	12 BI893295	BI893295 sai64a12.
14	189	75.3	582	12 BM731308	BM731308 sal70c07.
15	170.8	68.0	569	12 BM891461	BM891461 sam27f05.
16	162.2	64.6	554	10 BE609805	BE609805 sg42h06.y
17	160.6	64.0	632	10 BF425570	BF425570 su44d05.y
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19	146.8	58.5	185	13 BU764474	BU764474 sas02a05.
20	146.8	58.5	558	13 BQ253639	BQ253639 san63h08.
21	145.8	58.1	572	13 BU082080	BU082080 sar04e02.
22	145.2	57.8	579	12 BI471007	BI471007 sah92c08.
23	111.4	44.4	645	14 CA847674	CA847674 EST0582 t
24	100	39.8	564	12 BM085196	BM085196 saj33e03.
25	100	39.8	619	10 BF324448	BF324448 su24h10.y
26	76	30.3	252	10 BE806703	BE806703 ss64c12.y
27	76	30.3	480	10 BE806709	BE806709 ss64d06.y
28	76	30.3	532	10 BG507393	BG507393 sac58e10.
29	76	30.3	628	14 CA801562	CA801562 sau07f01.
30	76	30.3	736	14 CA801026	CA801026 sau23e06.
31	71.8	28.6	557	14 CD487105	CD487105 Gm ckr066
32	66.8	26.6	658	10 BG452436	BG452436 NF080D08L
33	66.2	26.4	451	14 CA800198	CA800198 sat79c06.
34	65.4	26.1	325	10 BE323370	BE323370 NF006F10P
35	65.4	26.1	635	10 BG456823	BG456823 NF097E07P
36	63.4	25.3	695	10 BG454886	BG454886 NF108F10L
37	63.2	25.2	605	10 BE347808	BE347808 sp05h06.y
38	60.2	24.0	679	13 BQ505113	BQ505113 EST612528
39	60.2	24.0	757	10 BG592948	BG592948 EST491626
40	59.2	23.6	412	10 BF324294	BF324294 su23c09.y
41	59.2	23.6	760	13 BQ993720	BQ993720 QGF5E17.y
42	58	23.1	387	10 AW929212	AW929212 EST338000
43	57.6	22.9	340	13 BU012727	BU012727 QGJ2L13.y
44	57.6	22.9	399	13 BU013957	BU013957 QGJ6A21.y
45	57.6	22.9	448	10 BG521765	BG521765 14-33 Ste

ALIGNMENTS

RESULT 1	BM891617	554 bp	mRNA	linear	EST 11-MAR-2002
LOCUS	sam41g03.y1	Gm-c1068	Glycine max	CDNA clone	SOYBEAN CLONE ID:
DEFINITION	Gm-c1068-7589	5'	similar to	TR:O82587	O82587 MTN3 HOMOLOG. ; , mRNA sequence.
ACCESSION	BM891617				
VERSION	BM891617.1				GI:19346737
KEYWORDS	EST.				
SOURCE	Glycine max (soybean)				
ORGANISM	Glycine max				
REFERENCE	1	(bases 1 to 554)			
AUTHORS	Shoemaker,R., Keim,P., Vodkin,L., Erpelding,J., Coryell,V., Khanna,A., Bolla,B., Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R. and Wilson,R.				
	Public Soybean EST Project				
TITLE	Unpublished				
JOURNAL	Contact: Shoemaker R/Public Soybean EST Project				
COMMENT	Public Soybean EST Project				
	Washington University School of Medicine				

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: est@watson.wustl.edu  
This clone is available through: ResGen, Invitrogen Corp. 2130  
South Memorial Parkway Huntville, AL 35801 For further information  
call: (800)-533-4363 or contact: ccu@resgen.com web site:  
www.resgen.com

Seq primer: -40RP from Gibco  
High quality sequence stop: 421.

FEATURES

source  
1. .554  
/organism="Glycine max"  
/mol\_type="mRNA"  
/db\_xref="taxon:3847"  
/clone="SOYBEAN CLONE ID: Gm-cl068-7589"  
/tissue\_type="Leaf, drought stressed, 1 month old plants,  
greenhouse grown"  
/lab\_host="DH10B"  
/clone\_lib="Gm-cl068"  
/note="Vector: pBluescript II SK+; Site 1: EcoRI; Site 2:  
XhoI; The cDNA library was constructed from mRNA isolated  
from drought stressed leaf tissue of the cultivar Williams  
82. The month old greenhouse grown plants were deprived of  
water for 3 days prior to harvesting the stressed leaf  
tissue. Complementary DNA was synthesized from mRNA using  
a primer consisting of a poly(dT) sequence with a XhoI  
restriction site. EcoRI adapters were ligated to the  
blunt-ended cDNA fragments followed by XhoI digestion. The  
cDNA fragments were directionally cloned into the  
EcoRI-XhoI restriction site of the pBluescript vector. The  
ligated cDNA fragments were transformed into DH10B host  
cells (GibcoBRL). This library was constructed in the  
laboratory of Dr. Randy Shoemaker."  
148 a 119 c 113 g 174 t

Query Match 84.5%; Score 212; DB 12; Length 554;  
Best Local Similarity 89.1%; Pred. No. 3e-43;  
Matches 212; Conservative 0; Mismatches 26; Indels 0; Gaps 0;  
13 GTGACACAGAAATTAAGCTAGAGCTTCATAGTTTCTTCTTCTCACCCTTCTCTC 72  
|||||  
1 GTGACACAGAAATTAAGCTAGAGCTTCATAGTTTCTTCTTCTCACCCTTCTCTC 60  
73 TCCCTTCAGACAAAGGGACAAAATCAGTGTGTGAGAGAGAGAGAAATTCACAAA 132  
|||||  
61 TCCCTTCAGACAAAGGGACAAAATCAGTGTGTGAGAGAGAGAGAAATTCACAAA 120  
133 CCATGTCCACAGTCATCTAAGTTTCGCCCTTTGGGATTCAGTAACATTGCCTCTCG 192  
|||||  
121 CCATGTCCACAGTCATCTAAGTTTCGCCCTTTGGGATTCAGTAACATTGCCTCTCG 180  
193 TGTGCTTCTTGGCACCACCTACCAACATTTTATAGAGTTTGTGAAGAAGANATCAACCGA 250  
|||||  
181 TGTGCTTCTTGGCACCACCTACCAACATTTTATAGAGTTTGTGAAGAAGANATCAACCGA 238

RESULT 2  
BM093555  
LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM

BM093555 575 bp mRNA linear EST 30-NOV-2001  
saj10ell.y1 Gm-cl066 Glycine max cDNA clone GENOME SYSTEMS CLONE  
ID: Gm-cl066-2517 5' similar to TR:082587 082587 MTN3 HOMOLOG. ; ,  
mRNA sequence.  
BM093555 GI:17022521  
EST.  
Glycine max (soybean)  
Glycine max  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids  
; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;  
Glycine.

REFERENCE  
AUTHORS  
1 (bases 1 to 575)  
Shoemaker,R., Keim,P., Vodkin,L., Erpelding,J., Coryell,V., Khanna  
A., Bolla,B., Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C.,  
Wyllie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers  
Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk  
R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann  
R., Waterston,R. and Wilson,R.  
Public Soybean EST Project  
Unpublished  
Contact: Shoemaker R/Public Soybean EST Project  
Public Soybean EST Project  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: est@watson.wustl.edu  
This clone is available through: ResGen, Invitrogen Corp. 2130  
South Memorial Parkway Huntville, AL 35801 For further information  
call: (800)-533-4363 or contact via email: ccu@resgen.com  
High quality sequence stop: 421.

FEATURES

source  
1. .575  
/organism="Glycine max"  
/mol\_type="mRNA"  
/db\_xref="taxon:3847"  
/clone="GENOME SYSTEMS CLONE ID: Gm-cl066-2517"  
/tissue\_type="Leaf and shoot tip, salt stressed, 2 week  
old seedling"  
/lab\_host="DH10B"  
/clone\_lib="Gm-cl066"  
/note="Vector: pBluescript II SK+; Site 1: EcoRI; Site 2:  
XhoI; The cDNA library was constructed from mRNA isolated  
from unexpanded leaves and the shoot tips of 2 week old  
seedling from the cultivar Williams. The 2 week old  
seedlings were salt stressed in a solution of 500mM NaCl  
for 3 days prior to harvesting. Complementary DNA was  
synthesized from mRNA using a primer consisting of a  
poly(dT) sequence with a XhoI restriction site. EcoRI  
adapters were ligated to the blunt-ended cDNA fragments  
followed by XhoI digestion. The cDNA fragments were  
directionally cloned into the EcoRI-XhoI restriction site  
of the pBluescript vector. The ligated cDNA fragments were  
transformed into DH10B host cells (GibcoBRL). This library  
was constructed in the laboratory of Dr. Randy  
Shoemaker."  
154 a 124 c 116 g 181 t

Query Match 84.5%; Score 212; DB 12; Length 575;  
Best Local Similarity 89.1%; Pred. No. 3e-43;  
Matches 212; Conservative 0; Mismatches 26; Indels 0; Gaps 0;  
13 GTGACACAGAAATTAAGCTAGAGCTTCATAGTTTCTTCTTCTCACCCTTCTCTC 72  
|||||  
1 GTGACACAGAAATTAAGCTAGAGCTTCATAGTTTCTTCTTCTCACCCTTCTCTC 60  
73 TCCCTTCAGACAAAGGGACAAAATCAGTGTGTGAGAGAGAGAGAAATTCACAAA 132  
|||||  
61 TCCCTTCAGACAAAGGGACAAAATCAGTGTGTGAGAGAGAGAGAAATTCACAAA 120  
133 CCATGTCCACAGTCATCTAAGTTTCGCCCTTTGGGATTCAGTAACATTGCCTCTCG 192  
|||||  
121 CCATGTCCACAGTCATCTAAGTTTCGCCCTTTGGGATTCAGTAACATTGCCTCTCG 180  
193 TGTGCTTCTTGGCACCACCTACCAACATTTTATAGAGTTTGTGAAGAAGANATCAACCGA 250  
|||||  
181 TGTGCTTCTTGGCACCACCTACCAACATTTTATAGAGTTTGTGAAGAAGANATCAACCGA 238

RESULT 3  
BU090931  
LOCUS  
DEFINITION  
BU090931 450 bp mRNA linear EST 29-AUG-2002  
su09e10.y1 Gm-cl066 Glycine max cDNA clone GENOME SYSTEMS CLONE ID:







/organism="Glycine max"  
/mol\_type="mRNA"  
/db\_xref="taxon:3847"  
/clone="SOYBEAN CLONE ID: Gm-cl057-2770"  
/tissue\_type="Degenerating cotyledons, 2 week old seedling"  
/lab\_host="DH10B"  
/clone\_lib="Gm-cl057"  
/note="Vector: pBluescript II SK+; Site 1: EcoRI; Site 2: XhoI; The cDNA library was constructed from mRNA isolated from degenerating cotyledons of 2 week old seedlings from PI468916. Complementary DNA was synthesized from mRNA using a primer consisting of a poly(dT) sequence with a XhoI restriction site. EcoRI adapters were ligated to the blunt-ended cDNA fragments followed by XhoI digestion. The cDNA fragments were directionally cloned into the EcoRI-XhoI restriction site of the pBluescript vector. The ligated cDNA fragments were transformed into DH10B host cells (GibcoBRL). This library was constructed in the laboratory of Dr. Randy Shoemaker."

BASE COUNT 156 a 124 c 119 g 181 t  
ORIGIN  
Query Match 79.7%; Score 200; DB 12; Length 580;  
Best Local Similarity 88.3%; Pred. No. 3.2e-40;  
Matches 212; Conservative 0; Mismatches 26; Indels 2; Gaps 1;  
y 13 GTGACACAGAAATTAAAGCTAGAGCTTCATAGTTCTTCTTTCTCACCTTCCTTCTC 72  
b 1 GTGACACAGAAATTAAAGCTAGAGCTTCATAGTTCTTCTTTCTCACCTTCCTTCTC 60  
y 73 TCCCTTCAGACAAAGGGACAAAAATC--NNNNNNNNNNNNNNNNNNNNNNNNNTTCCAA 130  
b 61 TCCCTTCAGACAAAGGGACAAAAATCAGTGTGTGAGAGAGAGAGAGAGAAATCCAA 120  
y 131 AACCATGTCCACAGTCATCTAAGTTTCGCCCTTTGGGATTCTAGGTAACATTGCCTCCTT 190  
b 121 AACCATGTCCACAGTCATCTAAGTTTCGCCCTTTGGGATTCTAGGTAACATTGCCTCCTT 180  
y 191 CGTGTGCTTTCTGGCACCACCTACCAACATTTTATAGAGTTTGTAGAAGANATCAACCGA 250  
b 181 CGTGTGCTTTCTGGCACCACCTACCAACATTTTATAGAGTTTGTAGAAGAAATCAACCGA 240

BF068522 389 bp mRNA linear EST 06-DEC-2001  
st83b03.y1 Gm-cl054 Glycine max cDNA clone GENOME SYSTEMS CLONE ID:  
Gm-cl054-845 5' similar to TR:P93332 P93332 MTN3 GENE PRECURSOR. ; ,  
mRNA sequence.  
BF068522  
BF068522.1 GI:10845385  
EST.  
Glycine max (soybean)  
Glycine max  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids  
; eurosids 1; Fabales; Fabaceae; Papilionoideae; Phaseoleae;  
Glycine.

1 (bases 1 to 389)  
Shoemaker,R., Keim,P., Vodkin,L., Erpelding,J., Coryell,V., Khanna  
,A., Bolla,B., Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C.,  
Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers  
,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk  
,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann  
,R., Waterston,R. and Wilson,R.  
Public Soybean EST Project  
Unpublished  
Contact: Shoemaker R/Public Soybean EST Project  
Public Soybean EST Project  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA  
Tel: 314 286 1800

Fax: 314 286 1810  
Email: est@watson.wustl.edu  
This clone is available through: Resgen, Invitrogen Corp. 2130  
South Memorial Parkway Huntsville, AL 35801 For further information  
call: (800)-533-4363 or contact via email: ccu@resgen.com  
Insert length: 1390 Std Error: 0.00  
High quality sequence stop: 346.  
Location/Qualifiers

FEATURES  
source  
1..389  
/organism="Glycine max"  
/mol\_type="mRNA"  
/db\_xref="taxon:3847"  
/clone="GENOME SYSTEMS CLONE ID: Gm-cl054-845"  
/tissue\_type="Leaf, 3 week old, greenhouse grown"  
/lab\_host="DH10B"  
/clone\_lib="Gm-cl054"  
/note="Vector: pBluescript II SK+; Site 1: EcoRI; Site 2:  
XhoI; The Harosoy NIL was constructed and seed was  
provided by Dr. J. Specht, University of Nebraska  
(Shoemaker and Specht, 1995). The cDNA library was  
constructed from mRNA isolated from leaf tissue at various  
developmental stages of 3 week old greenhouse grown  
plants. Complementary DNA was synthesized from mRNA using  
a primer consisting of a poly(dT) sequence with a XhoI  
restriction site and a 3' anchor. EcoRI adapters were  
ligated to the blunt-ended cDNA fragments followed by  
XhoI digestion. The cDNA fragments were directionally  
cloned into the EcoRI-XhoI restriction site of the  
pBluescript vector. The ligated cDNA fragments were  
transformed into DH10B host cells (GibcoBRL). This  
library was constructed in cooperation with Dr. Paul  
Keim's laboratory at Northern Arizona University."

BASE COUNT 106 a 89 c 73 g 120 t  
ORIGIN  
Query Match 77.3%; Score 194; DB 10; Length 389;  
Best Local Similarity 88.0%; Pred. No. 1.1e-38;  
Matches 206; Conservative 0; Mismatches 26; Indels 2; Gaps 1;  
QY 19 CAGAAATTAAGCTAGAGCTTCATAGTTTCTTCTTTCTCACCTTCCTTCTCCTT 78  
Db 2 CAGAAATTAAGCTAGAGCTTCATAGTTTCTTCTTTCTCACCTTCCTTCTCCTT 61  
QY 79 CAGACAAAGGGACAAAAATC--NNNNNNNNNNNNNNNNNNNNNNNNNTTCCAAACCAT 136  
Db 62 CAGACAAAGGGACAAAAATCAGTGTGTGAGAGAGAGAGAGAGAAATTCCAAACCAT 121  
QY 137 GTCCACAGTCATCTAAGTTTCGCCCTTTGGGATTCTAGGTAACATTGCCTTCGTGTG 196  
Db 122 GTCCACAGTCATCTAAGTTTCGCCCTTTGGGATTCTAGGTAACATTGCCTTCGTGTG 181  
QY 197 CTTTCTGGCACCACCTACCAACATTTTATAGAGTTTGTAGAAGANATCAACCGA 250  
Db 182 CTTTCTGGCACCACCTACCAACATTTTATAGAGTTTGTAGAAGAAATCAACCGA 235

RESULT 8  
BG041196  
LOCUS  
DEFINITION  
BG041196 457 bp mRNA linear EST 06-DEC-2001  
sv31a02.y1 Gm-cl057 Glycine max cDNA clone GENOME SYSTEMS CLONE ID:  
Gm-cl057-1155 5' similar to TR:082587 082587 MTN3 HOMOLOG. ; , mRNA  
sequence.  
BG041196  
BG041196.1 GI:12486992  
EST.  
Glycine max (soybean)  
Glycine max  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids  
; eurosids 1; Fabales; Fabaceae; Papilionoideae; Phaseoleae;  
Glycine.  
1 (bases 1 to 457)  
Shoemaker,R., Keim,P., Vodkin,L., Erpelding,J., Coryell,V., Khanna









/organism="Glycine max"  
/mol\_type="mrna"  
/db\_xref="taxon:3847"  
/clone="SOYBEAN CLONE ID: Gm-cl080-2434"  
/tissue\_type="Roots of 8 day old 'Bragg' supernodulating mutant NTS382 seedlings"  
/dev\_stage="8 days old"  
/lab\_host="DH10B"  
/clone\_lib="Gm-cl080"  
/note="Vector: pBluescript II SK+; Site\_1: EcoRI; Site\_2: XhoI; The mRNA was isolated from roots of 8 day old 'Bragg' supernodulating mutant NTS382 seedlings that were infected with Bradyrhizobium japonicum, strain USDA 110, 72 hours prior to harvest. Dr. Gary Stacey generously donated the tissue. The roots were flash-frozen in liquid nitrogen. Stratagene's cDNA Synthesis Kit (catalog number 200401) was used to synthesize the cDNA. First-strand synthesis was performed with 5-methyl dCTP, hence the ligated cDNA was hemimethylated. A modification of Stratagene's first-strand synthesis primer was used. An 'anchor' nucleotide (V=A, C, or G) was added to the 3' end of the primer [GAGAGAGAGAGAGAGAGAACTAGTCTCGAG(T)18V] to anchor the primer at the 5' end of the poly(A) tract. After second-strand synthesis, the cDNA ends were filled in with cloned Pfu DNA, ligated to EcoRI adapters and subsequently phosphorylated. The cDNA was then precipitated and redissolved in sterile, RNase-, DNase-free water. The XhoI site within the first- strand synthesis primer was then restricted by digestion with XhoI from Promega (40U/ul); all XhoI sites in the cDNA would be protected by their hemimethylated status. The cDNA constructs were size-fractionated with a 500bp cutoff, using Sephacryl S-500 High Resolution (Pharmacia Biotech) in a 2-mm diameter column and a bed volume of approximately 1ml. The column eluent was precipitated, redissolved, and ligated into Stratagene's pBluescript II XR Predigested vector (pBluescript II SK(+)) vector that has been digested with EcoRI and XhoI, and phosphorylated by Stratagene). This library was constructed in the laboratory of Dr. Paul Keim and Dr. Virginia H. Coryell at Northern Arizona University."  
BASE COUNT 155 a 128 c 123 g 187 t  
ORIGIN  
Query Match 76.1%; Score 191; DB 13; Length 593;  
Best Local Similarity 88.0%; Pred. No. 6e-38;  
Matches 191; Conservative 0; Mismatches 26; Indels 0; Gaps 0;  
2y 34 AGCTTCATAGTTCTCTCTTTCTCACCCTTCCTTCTCTCCCTTCAGACAAAGGGACAA 93  
|||  
Db 1 AGCTTCATAGTTCTCTCTTTCTCACCCTTCCTTCTCTCCCTTCAGACAAAGGGACAA 60  
2y 94 AAAATCNNNNNNNNNNNNNNNNNNNNNTTCCAAACCATGTCACAGTCATCTAA 153  
|||||  
Db 61 AAAATCAGTGTGTGAGAGAGAGAGAGAGAAATTCCAAACCATGTCACAGTCATCTAA 120  
2y 154 GTTTCGCCCTTTGGGATTCTAGGTAACATTGCTCCTCTCGTGTGCTTTCTGGCACCCTAC 213  
|||||  
Db 121 GTTTCGCCCTTTGGGATTCTAGGTAACATTGCTCCTCTCGTGTGCTTTCTGGCACCCTAC 180  
2y 214 CAACATTTTATAGATTGTGAAGAAGANATCAACCGA 250  
|||||  
Db 181 CAACATTTTATAGATTGTGAAGAAGAAATCAACCGA 217  
RESULT 12  
BU090543 458 bp mrna linear EST 29-AUG-2002  
LOCUS su06b06.y1 Gm-cl066 Glycine max cDNA clone GENOME SYSTEMS CLONE ID:  
DEFINITION Gm-cl066-827 5' similar to TR:082587 082587 MTN3 HOMOLOG. ;, mRNA  
sequence.  
ACCESSION BU090543  
VERSION BU090543.1 GI:22540700

KEYWORDS EST.  
SOURCE Glycine max (soybean)  
ORGANISM Glycine max  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids ; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.  
REFERENCE 1 (bases 1 to 458)  
AUTHORS Shoemaker,R., Keim,P., Vodkin,L., Erpelding,J., Coryell,V., Khanna ,A., Bolla,B., Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers ,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk ,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann ,R., Waterston,R. and Wilson,R.  
TITLE Public Soybean EST Project  
JOURNAL Unpublished  
COMMENT Contact: Shoemaker R/Public Soybean EST Project  
Public Soybean EST Project  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: est@watson.wustl.edu  
This clone is available through: Genome Systems, Inc. 4633 World Parkway Circle St. Louis, Missouri 63134 For further information call: (800) 430-0030 or (314) 427-3222 FAX:(888) 919-3324 or (314) 427-3324 or contact: clones@genomesystems.com or info@genomesystems.com web site: www.genomesystems.com  
High quality sequence stop: 421.  
Location/Qualifiers  
1. .458  
/organism="Glycine max"  
/mol\_type="mrna"  
/db\_xref="taxon:3847"  
/clone="GENOME SYSTEMS CLONE ID: Gm-cl066-827"  
/tissue\_type="Leaf and shoot tip, salt stressed, 2 week old seedling"  
/lab\_host="DH10B"  
/clone\_lib="Gm-cl066"  
/note="Vector: pBluescript II SK+; Site\_1: EcoRI; Site\_2: XhoI; The cDNA library was constructed from mRNA isolated from unexpanded leaves and the shoot tips of 2 week old seedling from the cultivar Williams. The 2 week old seedlings were salt stressed in a solution of 500mM NaCl for 3 days prior to harvesting. Complementary DNA was synthesized from mRNA using a primer consisting of a poly(dT) sequence with a XhoI restriction site. EcoRI adapters were ligated to the blunt-ended cDNA fragments followed by XhoI digestion. The cDNA fragments were directionally cloned into the EcoRI-XhoI restriction site of the pBluescript vector. The ligated cDNA fragments were transformed into DH10B host cells (GibcoBRL). This library was constructed in the laboratory of Dr. Randy Shoemaker."  
BASE COUNT 122 a 97 c 93 g 144 t 2 others  
ORIGIN  
Query Match 75.8%; Score 190.2; DB 13; Length 458;  
Best Local Similarity 84.6%; Pred. No. 9.6e-38;  
Matches 208; Conservative 0; Mismatches 35; Indels 3; Gaps 1;  
Qy 8 GTTGTGTGACACAGAAATTAAGCTAGAGCTTCATAGTTCTTCTTTTCTCACCTTCC 67  
|||  
Db 2 GTTGTGTGACACAGAAATTAAGCTAGAGCTTCATAGTTCTTCTTTTCTCACCTTCC 61  
Qy 68 TTCTCTCCCTTCAGACAAAGGGACAAAATCNCNNNNNNNNNNNNNNNNNNNNNTTC 127  
|||  
Db 62 TTCTCTCCCTTCAGACAAAGGGACAAAATCAGTGTGTGAGAGAGAGAGAGAAATTC 121  
Qy 128 CAAAACCATGTCCACAGTCATCTAAGTTTCGCCTTTGGGATTCTAGTAACATTGCCTC 187  
|||  
Db 122 CAAAACCATGTCCACAGTCATCTAAGTTTCGCCTTTGGGATTCTAGTAACATTGCCT 181



CDNA fragments were directionally cloned into the EcoRI-XhoI restriction site of the pBluescript vector. The ligated cDNA fragments were transformed into DH10B host cells (GibcoBRL). This library was constructed in the laboratory of Dr. Randy Shoemaker."

BASE COUNT 154 a 124 c 122 g 182 t  
ORIGIN  
Query Match 75.3%; Score 189; DB 12; Length 582;  
Best Local Similarity 87.9%; Pred. No. 1.9e-37;  
Matches 189; Conservative 0; Mismatches 26; Indels 0; Gaps 0;  
QY 36 CTTTCATAGTTTCTTCTTCTTCTCACCTTCCTTCTCTCCCTTCAGACAAAGGGACAAA 95  
Db 1 CTTTCATAGTTTCTTCTTCTTCTCACCTTCCTTCTCTCCCTTCAGACAAAGGGACAAA 60  
QY 96 AATCNNNNNNNNNNNNNNNNNNNNNTTCCAAACCATGTCCACAGTCATCTAAGT 155  
Db 61 AATCAGTGTGTGACAGAGAGAGAGAGAGAAATCCAAACCATGTCCACAGTCATCTAAGT 120  
QY 156 TTGGCCTTTGGGATCTTAGGTAACATTGCTTCCTTCCTCGTGTGCTTTTGGCACCACCTACCA 215  
Db 121 TTGGCCTTTGGGATCTTAGGTAACATTGCTTCCTTCCTCGTGTGCTTTTGGCACCACCTACCA 180  
QY 216 ACATTTTATAGAGTTTGTAAGAAGANATCAACCGA 250  
Db 181 ACATTTTATAGAGTTTGTAAGAAGAAATCAACCGA 215

RESULT 15  
BM891461  
LOCUS  
DEFINITION  
sam27f05.y1 Gm-cl068 Glycine max cDNA clone SOYBEAN CLONE ID:  
Gm-cl068-6033 5' similar to TR:082587 O82587 MTN3 HOMOLOG. ;, mRNA  
sequence.  
BM891461  
BM891461.1 GI:19346581  
EST.  
Glycine max (soybean)  
Glycine max  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids  
; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;  
Glycine.  
1 (bases 1 to 569)

REFERENCE  
AUTHORS  
Shoemaker, R., Keim, P., Vodkin, L., Erpelding, J., Coryell, V., Khanna  
A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C.,  
Wyllie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers  
Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk  
R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann  
R., Waterston, R. and Wilson, R.  
Public Soybean EST Project  
Unpublished  
Contact: Shoemaker R/Public Soybean EST Project  
Public Soybean EST Project  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: est@watson.wustl.edu  
This clone is available through: ResGen, Invitrogen Corp. 2130  
South Memorial Parkway Huntsville, AL 35801 For further information  
call: (800)-533-4363 or contact: ccu@resgen.com web site:  
www.resgen.com  
Seg primer: -40RP from Gibco  
High quality sequence stop: 457.  
Location/Qualifiers  
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greenhouse grown"  
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/clone\_lib="Gm-cl068"  
/note="Vector: pBluescript II SK+; Site 1: EcoRI; Site 2:  
XhoI; The cDNA library was constructed from mRNA isolated  
from drought stressed leaf tissue of the cultivar Williams  
82. The month old greenhouse grown plants were deprived of  
water for 3 days prior to harvesting the stressed leaf  
tissue. Complementary DNA was synthesized from mRNA using  
a primer consisting of a poly(dT) sequence with a XhoI  
restriction site. EcoRI adapters were ligated to the  
blunt-ended cDNA fragments followed by XhoI digestion. The  
cDNA fragments were directionally cloned into the  
EcoRI-XhoI restriction site of the pBluescript vector. The  
ligated cDNA fragments were transformed into DH10B host  
cells (GibcoBRL). This library was constructed in the  
laboratory of Dr. Randy Shoemaker."  
BASE COUNT 163 a 121 c 101 g 184 t  
ORIGIN

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Best Local Similarity 86.4%; Pred. No. 7.6e-33;  
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Db 181 TGTGCTTTCTGGCTCCTCT 199

Search completed: November 6, 2003, 04:11:02  
Job time : 1399 secs

GenCore version 5.1.6  
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run on: November 6, 2003, 03:46:49 ; Search time 1410 Seconds  
(without alignments)  
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8: gb\_pl:\*  
9: gb\_pr:\*  
10: gb\_ro:\*  
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13: gb\_un:\*  
14: gb\_vi:\*  
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17: em\_hum:\*  
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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

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5	35	13.9	69702	2	AC027743	AC027743 Homo sapi
6	35	13.9	70125	2	AC087705	AC087705 Homo sapi
C 7	35	13.9	136479	2	AC144333	AC144333 Macaca mu
C 8	35	13.9	140055	2	AP005013	AP005013 Homo sapi
9	35	13.9	158231	2	AC093306	AC093306 Homo sapi
C 10	35	13.9	160191	2	AC124963	AC124963 Medicago
C 11	35	13.9	178521	2	AC126450	AC126450 Mus muscu
C 12	35	13.9	185479	2	AP001484	AP001484 Homo sapi
13	35	13.9	230154	2	AC140686	AC140686 Rattus no
C 14	35	13.9	236385	2	AC094936	AC094936 Rattus no
C 15	35	13.9	241607	2	AC113636	AC113636 Rattus no
C 16	35	13.9	281605	2	AC095329	AC095329 Rattus no
17	34	13.5	45794	2	AC015492	AC015492 Homo sapi
C 18	34	13.5	52271	2	AC137720	AC137720 Homo sapi
19	34	13.5	61577	2	AC083754	AC083754 Homo sapi
20	34	13.5	62157	2	AC084304	AC084304 Homo sapi
C 21	34	13.5	64668	2	AC101190	AC101190 Mus muscu
C 22	34	13.5	64836	2	AC100068	AC100068 Mus muscu
C 23	34	13.5	65557	2	AC106855	AC106855 Homo sapi
24	34	13.5	65594	2	AC101226	AC101226 Mus muscu
25	34	13.5	66301	2	AC090550	AC090550 Homo sapi
C 26	34	13.5	67690	2	AC123781	AC123781 Homo sapi
27	34	13.5	68171	2	AC100157	AC100157 Mus muscu
C 28	34	13.5	108913	2	AC025024	AC025024 Homo sapi
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C 31	34	13.5	113851	2	AP000571	AP000571 Homo sapi
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C 33	34	13.5	119714	2	AC073028	AC073028 Homo sapi
C 34	34	13.5	132605	2	AC023450	AC023450 Homo sapi
C 35	34	13.5	164208	2	AC133383	AC133383 Rattus no
36	34	13.5	165147	2	AC021342	AC021342 Homo sapi
37	34	13.5	180171	2	AC119771	AC119771 Rattus no
38	34	13.5	181504	2	AP001100	AP001100 Homo sapi
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C 40	34	13.5	187411	2	AC115565	AC115565 Rattus no
C 41	34	13.5	201427	2	AC127843	AC127843 Rattus no
42	34	13.5	204563	2	AC115257	AC115257 Rattus no
43	34	13.5	213666	2	AC020837	AC020837 Mus muscu
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C 45	34	13.5	221389	2	AC112122	AC112122 Rattus no
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C 60	34	13.5	266038	2	AC128025	AC128025 Rattus no
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62	33	13.1	1521	8	AF382747	AF382747 Cavendish
C 63	33	13.1	2585	8	AF142683	AF142683 Baphia ma
C 64	33	13.1	12269	3	AF374374	AF374374 Oikopleur
C 65	33	13.1	25837	2	AC087198	AC087198 Homo sapi



C 66	33	13.1	29359	2	AP001083	AP001083 Homo sapi	139	33	13.1	88037	2	PFMAL13P8	AL096782 Plasmodiu
C 67	33	13.1	29716	2	AC103823	AC103823 Homo sapi	140	33	13.1	89376	2	AC139073	AC139073 Homo sapi
C 68	33	13.1	33240	2	CEH40008	Z93095 Caenorhabdi	141	33	13.1	91334	2	AC024691	AC024691 Homo sapi
C 69	33	13.1	35692	2	AC067862	AC067862 Homo sapi	c 142	33	13.1	94153	2	AC139443	AC139443 Rattus no
C 70	33	13.1	44437	2	AC100102	AC100102 Mus muscu	c 143	33	13.1	99305	2	AC120578	Continuation (4 of
C 71	33	13.1	44876	2	AC100114	AC100114 Mus muscu	c 144	33	13.1	100392	2	AP002737	AP002737 Homo sapi
C 72	33	13.1	45050	2	AC100277	AC100277 Mus muscu	c 145	33	13.1	103408	2	AL606524	AL606524 Homo sapi
C 73	33	13.1	45633	2	AC011630	AC011630 Homo sapi	146	33	13.1	105469	2	AC138215	AC138215 Homo sapi
C 74	33	13.1	47269	2	AC068834	AC068834 Homo sapi	c 147	33	13.1	105791	2	AC095467	Continuation (4 of
C 75	33	13.1	47436	2	AC106032	AC106032 Homo sapi	148	33	13.1	107448	2	DMBR41K5	AL121843 Drosophil
C 76	33	13.1	49738	2	AC015752	AC015752 Homo sapi	c 149	33	13.1	108821	2	AC138182	AC138182 Homo sapi
C 77	33	13.1	50531	2	AC100970	AC100970 Mus muscu	150	33	13.1	109097	2	AC013377	AC013377 Homo sapi
C 78	33	13.1	50551	2	AC101140	AC101140 Mus muscu	c 151	33	13.1	110000	2	AC098035	Continuation (4 of
C 79	33	13.1	51531	2	AC115089	AC115089 Homo sapi	152	33	13.1	110000	2	AC107134	Continuation (3 of
C 80	33	13.1	52375	2	AC087052	AC087052 Homo sapi	c 153	33	13.1	110000	2	AC111970	Continuation (3 of
C 81	33	13.1	52453	2	AC116153	AC116153 Homo sapi	c 154	33	13.1	110000	2	AC112374	Continuation (4 of
C 82	33	13.1	54099	2	AC079963	AC079963 Homo sapi	155	33	13.1	110000	2	AC114698	Continuation (4 of
C 83	33	13.1	54634	2	AC132201	AC132201 Homo sapi	c 156	33	13.1	110000	2	AC125151	Continuation (3 of
C 84	33	13.1	54958	2	AC103850	AC103850 Homo sapi	157	33	13.1	110000	2	AC126295	Continuation (3 of
C 85	33	13.1	56448	2	AC101445	AC101445 Ciona sav	c 158	33	13.1	110000	2	AC021644	AC021644 Homo sapi
C 86	33	13.1	56983	2	AC068830	AC068830 Homo sapi	159	33	13.1	110000	2	AC141230	AC141230 Homo sapi
C 87	33	13.1	57175	2	AC100243	AC100243 Mus muscu	160	33	13.1	110000	2	AC141230	Continuation (3 of
C 88	33	13.1	57335	2	AC115739	AC115739 Mus muscu	c 161	33	13.1	110720	2	AC138189	AC138189 Mus muscu
C 89	33	13.1	58250	2	AC103690	AC103690 Homo sapi	c 162	33	13.1	115036	2	AP000444	AP000444 Homo sapi
C 90	33	13.1	58852	2	AC036190	AC036190 Homo sapi	c 163	33	13.1	118218	2	AP000670	AP000670 Homo sapi
C 91	33	13.1	59369	2	AC115765	AC115765 Mus muscu	164	33	13.1	119419	2	AP000666	AP000666 Homo sapi
C 92	33	13.1	59703	2	AC100704	AC100704 Mus muscu	165	33	13.1	121774	2	AC084059	AC084059 Mus muscu
C 93	33	13.1	59866	2	AC100572	AC100572 Mus muscu	c 166	33	13.1	124696	2	AP000649	AP000649 Homo sapi
C 94	33	13.1	60540	2	AC100489	AC100489 Mus muscu	167	33	13.1	128915	2	AC068465	AC068465 Homo sapi
C 95	33	13.1	60803	2	AC102309	AC102309 Mus muscu	c 168	33	13.1	132374	2	AC026503	AC026503 Homo sapi
C 96	33	13.1	61101	2	AC083975	AC083975 Homo sapi	c 169	33	13.1	132451	2	AC140788	AC140788 Mus muscu
C 97	33	13.1	61352	2	AC099964	AC099964 Mus muscu	170	33	13.1	134237	2	AC126501	AC126501 Rattus no
C 98	33	13.1	61375	2	AC068267	AC068267 Homo sapi	171	33	13.1	134867	2	AC013788	AC013788 Homo sapi
C 99	33	13.1	61502	2	AC015619	AC015619 Homo sapi	c 172	33	13.1	137309	2	AC138008	AC138008 Oryza sat
C 100	33	13.1	62550	2	AC090460	AC090460 Homo sapi	173	33	13.1	137488	2	AC025401	AC025401 Homo sapi
C 101	33	13.1	63084	2	AC100619	AC100619 Mus muscu	c 174	33	13.1	140819	2	AC012418	AC012418 Homo sapi
C 102	33	13.1	63125	2	AC134783	AC134783 Homo sapi	c 175	33	13.1	140954	2	AC141538	AC141538 Rattus no
C 103	33	13.1	63192	2	AC135071	AC135071 Homo sapi	c 176	33	13.1	141281	2	AC018955	AC018955 Mus muscu
C 104	33	13.1	63349	2	AC102470	AC102470 Mus muscu	c 177	33	13.1	141710	2	AP006167	AP006167 Oryza sat
C 105	33	13.1	63513	2	AC074061	AC074061 Homo sapi	c 178	33	13.1	141854	2	AC021595	AC021595 Homo sapi
C 106	33	13.1	64323	2	AC015838	AC015838 Homo sapi	179	33	13.1	143239	2	AP005285	AP005285 Oryza sat
C 107	33	13.1	64958	2	AC090905	AC090905 Homo sapi	180	33	13.1	143680	2	AC136539	AC136539 Rattus no
C 108	33	13.1	64970	2	AC099958	AC099958 Mus muscu	181	33	13.1	144037	2	RN141K6	AL603724 Rattus no
C 109	33	13.1	65300	2	AC134677	AC134677 Homo sapi	c 182	33	13.1	145089	2	AC027093	AC027093 Homo sapi
C 110	33	13.1	65762	2	AC079913	AC079913 Homo sapi	c 183	33	13.1	145710	2	AP000809	AP000809 Homo sapi
C 111	33	13.1	66015	2	AC009339	AC009339 Drosophil	184	33	13.1	147168	2	AC080067	AC080067 Homo sapi
C 112	33	13.1	67338	2	AC090600	AC090600 Homo sapi	c 185	33	13.1	147184	2	AC135778	AC135778 Homo sapi
C 113	33	13.1	67440	2	AC084138	AC084138 Homo sapi	186	33	13.1	147489	2	AP001926	AP001926 Homo sapi
C 114	33	13.1	68305	2	AC101607	AC101607 Mus muscu	c 187	33	13.1	148312	2	AP001886	AP001886 Homo sapi
C 115	33	13.1	68373	2	AC115101	AC115101 Homo sapi	c 188	33	13.1	148772	2	AC055826	AC055826 Homo sapi
C 116	33	13.1	68882	2	AC101569	AC101569 Mus muscu	c 189	33	13.1	149856	2	AC021411	AC021411 Homo sapi
C 117	33	13.1	68912	2	AC01508	AC101508 Mus muscu	c 190	33	13.1	150399	2	AC015784	AC015784 Homo sapi
C 118	33	13.1	69770	6	AX647131	AX647131 Sequence	c 191	33	13.1	151386	2	AC013312	AC013312 Homo sapi
C 119	33	13.1	69843	2	AC025903	AC025903 Homo sapi	192	33	13.1	151552	2	AC023437	AC023437 Homo sapi
C 120	33	13.1	70439	2	AC079291	AC079291 Homo sapi	193	33	13.1	152468	2	AP001584	AP001584 Homo sapi
C 121	33	13.1	70471	2	AC130348	AC130348 Homo sapi	194	33	13.1	152728	2	AC128285	AC128285 Rattus no
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C 123	33	13.1	71256	2	AC105011	AC105011 Homo sapi	c 196	33	13.1	154158	2	AL365257	AL365257 Homo sapi
C 124	33	13.1	71824	2	AC015759	AC015759 Homo sapi	197	33	13.1	155194	2	AC025231	AC025231 Homo sapi
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C 126	33	13.1	72757	2	AC025301	AC025301 Homo sapi	c 199	33	13.1	155388	2	AC139326	AC139326 Mus muscu
C 127	33	13.1	72807	2	AC023525	AC023525 Homo sapi	c 200	33	13.1	155600	2	AC134601	AC134601 Mus muscu
C 128	33	13.1	72907	2	AC016010	AC016010 Homo sapi	201	33	13.1	155958	2	AC127424	AC127424 Magnaport
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C 130	33	13.1	73639	2	AC055834	AC055834 Homo sapi	203	33	13.1	158996	2	AP000791	AP000791 Homo sapi
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C 138	33	13.1	87526	2	AC018485	AC018485 Drosophil	211	33	13.1	164420	2	AC023323	AC023323 Homo sapi



C 212	33	13.1	164655	2	AC080134	AC080134 Homo sapi
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c 227	33	13.1	171006	2	AP002504	AP002504 Homo sapi
c 228	33	13.1	172921	2	AP002454	AP002454 Homo sapi
c 229	33	13.1	173657	2	AP001014	AP001014 Homo sapi
c 230	33	13.1	174203	2	AC141570	AC141570 Rattus no
c 231	33	13.1	174280	2	AC011077	AC011077 Homo sapi
232	33	13.1	174327	2	AL672191	AL672191 Homo sapi
c 233	33	13.1	174383	2	AC012053	AC012053 Homo sapi
c 234	33	13.1	174894	2	AC123915	AC123915 Mus muscu
c 235	33	13.1	175980	2	AC025082	AC025082 Homo sapi
c 236	33	13.1	176331	2	AL831747	AL831747 Danio rer
c 237	33	13.1	176578	2	AC041008	AC041008 Homo sapi
c 238	33	13.1	177443	2	AP001164	AP001164 Homo sapi
c 239	33	13.1	177660	2	AC141656	AC141656 Rattus no
c 240	33	13.1	177716	2	AP001027	AP001027 Homo sapi
241	33	13.1	178478	2	AP002834	AP002834 Homo sapi
c 242	33	13.1	179843	2	AP001272	AP001272 Homo sapi
c 243	33	13.1	180273	2	AP002894	AP002894 Homo sapi
c 244	33	13.1	180291	2	AC020711	AC020711 Homo sapi
245	33	13.1	180354	2	AC009689	AC009689 Homo sapi
246	33	13.1	180962	2	AC068917	AC068917 Homo sapi
247	33	13.1	181254	2	AP000825	AP000825 Homo sapi
c 248	33	13.1	181360	2	AC132844	AC132844 Mus muscu
c 249	33	13.1	181515	2	AC119068	AC119068 Canis fam
250	33	13.1	181805	2	AC114445	AC114445 Rattus no
251	33	13.1	182928	2	AP001161	AP001161 Homo sapi
c 252	33	13.1	184513	2	AC024433	AC024433 Homo sapi
253	33	13.1	185195	2	AC074001	AC074001 Homo sapi
254	33	13.1	185644	2	AL391723	AL391723 Homo sapi
c 255	33	13.1	187214	2	AC121384	AC121384 Rattus no
c 256	33	13.1	188088	2	AC137982	AC137982 Mus muscu
c 257	33	13.1	188514	2	AC104554	AC104554 Mus muscu
c 258	33	13.1	188565	2	AC125250	AC125250 Mus muscu
c 259	33	13.1	189623	2	AC018640	AC018640 Homo sapi
260	33	13.1	190105	2	AC140255	AC140255 Mus muscu
c 261	33	13.1	190886	2	AC125079	AC125079 Mus muscu
c 262	33	13.1	191020	2	AC090758	AC090758 Homo sapi
c 263	33	13.1	191196	2	AL441903	AL441903 Homo sapi
c 264	33	13.1	191564	2	AC139653	AC139653 Rattus no
c 265	33	13.1	193433	2	AP001523	AP001523 Homo sapi
c 266	33	13.1	193787	2	AP000774	AP000774 Homo sapi
c 267	33	13.1	195029	2	AC007902	AC007902 Homo sapi
268	33	13.1	195419	2	AP005132	AP005132 Homo sapi
269	33	13.1	196252	2	BX324145	BX324145 Danio rer
c 270	33	13.1	196511	2	AP000854	AP000854 Homo sapi
271	33	13.1	196933	2	AC079854	AC079854 Homo sapi
c 272	33	13.1	197295	2	AC139652	AC139652 Rattus no
c 273	33	13.1	197866	2	AC068293	AC068293 Homo sapi
c 274	33	13.1	198136	2	AC090165	AC090165 Homo sapi
275	33	13.1	200000	2	AC004618	AC004618 Homo sapi
c 276	33	13.1	200135	2	AC121046	AC121046 Rattus no
277	33	13.1	202217	2	AC116730	AC116730 Mus muscu
c 278	33	13.1	208497	2	AC127844	AC127844 Rattus no
c 279	33	13.1	208657	2	AC046179	AC046179 Homo sapi
280	33	13.1	210147	2	BX294157	BX294157 Danio rer
281	33	13.1	210876	2	AC098466	AC098466 Rattus no
282	33	13.1	212309	2	AC141534	AC141534 Rattus no
c 283	33	13.1	215201	2	BX294007	BX294007 Mus muscu
284	33	13.1	215315	2	AC107671	AC107671 Mus muscu

285	33	13.1	217203	2	AC139956	AC139956 Rattus no
c 286	33	13.1	218963	2	AC131850	AC131850 Rattus no
287	33	13.1	220507	2	AC098007	AC098007 Rattus no
288	33	13.1	220867	2	AC094006	AC094006 Rattus no
c 289	33	13.1	222378	2	AC015862	AC015862 Homo sapi
c 290	33	13.1	222477	2	AP001847	AP001847 Homo sapi
c 291	33	13.1	223151	2	AC098029	AC098029 Rattus no
292	33	13.1	224788	2	AP001905	AP001905 Homo sapi
293	33	13.1	225230	2	AC022235	AC022235 Mus muscu
c 294	33	13.1	229822	2	AC138642	AC138642 Mus muscu
295	33	13.1	230620	2	AC109649	AC109649 Rattus no
c 296	33	13.1	230703	2	AC120663	AC120663 Rattus no
297	33	13.1	231349	2	AC138617	AC138617 Mus muscu
c 298	33	13.1	231698	2	AC118117	AC118117 Rattus no
c 299	33	13.1	233428	2	AC011064	AC011064 Drosophil
300	33	13.1	234844	2	AC111734	AC111734 Rattus no
c 301	33	13.1	235151	2	AC125640	AC125640 Rattus no
c 302	33	13.1	235333	2	AC109551	AC109551 Rattus no
303	33	13.1	236646	2	AC142152	AC142152 Rattus no
c 304	33	13.1	240262	2	AC137467	AC137467 Rattus no
c 305	33	13.1	240396	2	AC138343	AC138343 Mus muscu
c 306	33	13.1	241730	2	AC103283	AC103283 Rattus no
307	33	13.1	242915	2	AC117981	AC117981 Rattus no
c 308	33	13.1	243887	2	AC024898	AC024898 Homo sapi
309	33	13.1	244010	2	AC105848	AC105848 Rattus no
310	33	13.1	244224	2	AC125992	AC125992 Rattus no
c 311	33	13.1	244477	2	AC131832	AC131832 Rattus no
c 312	33	13.1	246083	2	AC106313	AC106313 Rattus no
c 313	33	13.1	246212	2	AC109769	AC109769 Rattus no
314	33	13.1	246680	2	AC094910	AC094910 Rattus no
c 315	33	13.1	252370	2	AC117214	AC117214 Mus muscu
c 316	33	13.1	252825	2	AC132024	AC132024 Rattus no
317	33	13.1	253176	2	AC094477	AC094477 Rattus no
c 318	33	13.1	253787	2	AC130832	AC130832 Mus muscu
c 319	33	13.1	256093	2	AC105672	AC105672 Rattus no
c 320	33	13.1	256473	2	AC109689	AC109689 Rattus no
321	33	13.1	256528	2	AC108270	AC108270 Rattus no
c 322	33	13.1	257178	2	AC114088	AC114088 Rattus no
c 323	33	13.1	258520	2	AC135085	AC135085 Mus muscu
324	33	13.1	265352	2	AC095748	AC095748 Rattus no
c 325	33	13.1	266617	2	AC124879	AC124879 Rattus no
326	33	13.1	267137	2	AC098319	AC098319 Rattus no
327	33	13.1	270567	2	AC138086	AC138086 Homo sapi
328	33	13.1	270706	2	AC129862	AC129862 Rattus no
c 329	33	13.1	271496	2	AC142073	AC142073 Rattus no
c 330	33	13.1	277226	2	AC105691	AC105691 Rattus no
331	33	13.1	278521	2	AC092715	AC092715 Homo sapi
332	33	13.1	285107	2	AC103104	AC103104 Rattus no
c 333	33	13.1	292173	2	BX294381	BX294381 Danio rer
334	33	13.1	301662	2	AC127291	AC127291 Mus muscu
c 335	33	13.1	310448	2	AC131354	AC131354 Rattus no
336	33	13.1	318589	2	AC120476	AC120476 Rattus no
337	33	13.1	319335	2	AC106226	AC106226 Rattus no
c 338	33	13.1	323417	2	AC109009	AC109009 Rattus no
c 339	33	13.1	327654	2	AC020816	AC020816 Mus muscu
340	33	13.1	329577	2	AC128988	AC128988 Rattus no
c 341	33	13.1	338462	2	BX465196	BX465196 Mus muscu
c 342	33	13.1	342774	2	AC116082	AC116082 Rattus no
c 343	33	13.1	348465	2	AC131165	AC131165 Rattus no
344	32	12.7	263	11	G41076	G41076 C14M20 Plas
345	32	12.7	735	8	AY101159	AY101159 Cordisepa
346	32	12.7	10835	8	AY146811	AY146811 Zea mays
347	32	12.7	23489	2	AC091079	AC091079 Homo sapi
348	32	12.7	32926	2	AL354742	AL354742 Homo sapi
c 349	32	12.7	35284	2	CEH27E01	Z92799 Caenorhabdi
c 350	32	12.7	36608	2	AC104227	AC104227 Homo sapi
351	32	12.7	38360	2	AC087400	AC087400 Homo sapi
352	32	12.7	38428	2	AC145166	AC145166 Homo sapi
c 353	32	12.7	43295	2	AC024381	AC024381 Homo sapi
c 354	32	12.7	43963	2	AC104243	AC104243 Homo sapi
355	32	12.7	44433	2	AC110052	AC110052 Homo sapi
356	32	12.7	44465	2	AC025007	AC025007 Homo sapi
357	32	12.7	44693	2	AC087338	AC087338 Homo sapi

358	32	12.7	47483	2	AC141834	AC141834 Apis mell	C 431	32	12.7	67951	2	AC102112	AC102112 Mus muscu
359	32	12.7	47760	6	AX059454	AX059454 Sequence	432	32	12.7	67984	2	AC118190	AC118190 Mus muscu
c 360	32	12.7	48864	2	AC060774	AC060774 Homo sapi	C 433	32	12.7	68074	2	AC101494	AC101494 Mus muscu
361	32	12.7	49688	2	AC090162	AC090162 Homo sapi	434	32	12.7	68087	2	AC023856	AC023856 Homo sapi
c 362	32	12.7	50994	2	AC104591	AC104591 Homo sapi	C 435	32	12.7	68326	2	AC055793	AC055793 Mus muscu
c 363	32	12.7	51896	2	AC068031	AC068031 Homo sapi	C 436	32	12.7	68407	2	AC048372	AC048372 Homo sapi
364	32	12.7	52226	2	AC107902	AC107902 Homo sapi	437	32	12.7	68445	2	AC124257	AC124257 Homo sapi
c 365	32	12.7	52915	2	AC127531	AC127531 Homo sapi	C 438	32	12.7	68451	2	AC110061	AC110061 Homo sapi
c 366	32	12.7	53735	2	AC101365	AC101365 Mus muscu	439	32	12.7	68630	2	AC090468	AC090468 Homo sapi
c 367	32	12.7	54188	2	AC100937	AC100937 Mus muscu	440	32	12.7	68999	2	AC100684	AC100684 Mus muscu
c 368	32	12.7	54296	2	AC119232	AC119232 Mus muscu	C 441	32	12.7	69161	2	AC101153	AC101153 Mus muscu
369	32	12.7	54606	2	AC100097	AC100097 Mus muscu	C 442	32	12.7	69337	2	AC101261	AC101261 Mus muscu
c 370	32	12.7	55496	2	AC100480	AC100480 Mus muscu	443	32	12.7	69354	2	AC069342	AC069342 Homo sapi
371	32	12.7	55772	2	AC114339	AC114339 Homo sapi	444	32	12.7	70183	2	AC090566	AC090566 Homo sapi
372	32	12.7	55956	2	AC101559	AC101559 Mus muscu	C 445	32	12.7	70282	2	AC111072	AC111072 Mus muscu
373	32	12.7	56213	2	AC106023	AC106023 Homo sapi	C 446	32	12.7	70508	2	AC016784	AC016784 Homo sapi
374	32	12.7	56264	2	AC100886	AC100886 Mus muscu	C 447	32	12.7	70589	2	AC087515	AC087515 Homo sapi
c 375	32	12.7	56690	2	AC100882	AC100882 Mus muscu	448	32	12.7	70751	2	AC101724	AC101724 Mus muscu
c 376	32	12.7	57286	2	AC117683	AC117683 Mus muscu	C 449	32	12.7	70798	2	AC024273	AC024273 Homo sapi
c 377	32	12.7	57865	2	AC101541	AC101541 Ciona sav	C 450	32	12.7	70864	2	AC101195	AC101195 Mus muscu
378	32	12.7	58496	2	AC101077	AC101077 Mus muscu	451	32	12.7	71063	2	AC027580	AC027580 Homo sapi
379	32	12.7	58569	2	AC134424	AC134424 Homo sapi	452	32	12.7	71353	2	AC135175	AC135175 Homo sapi
c 380	32	12.7	58657	2	AC101030	AC101030 Mus muscu	C 453	32	12.7	71491	2	AC124619	AC124619 Mus muscu
381	32	12.7	59008	2	AC100379	AC100379 Mus muscu	454	32	12.7	71496	2	AC090722	AC090722 Homo sapi
382	32	12.7	59199	2	AC132848	AC132848 Mus muscu	455	32	12.7	71508	2	AC101219	AC101219 Mus muscu
c 383	32	12.7	59413	2	AC136535	AC136535 Rattus no	456	32	12.7	71662	2	AC027786	AC027786 Homo sapi
384	32	12.7	59446	2	AC099952	AC099952 Mus muscu	C 457	32	12.7	71704	2	AC068468	AC068468 Homo sapi
c 385	32	12.7	59747	2	AC069053	AC069053 Homo sapi	458	32	12.7	71920	2	AC105200	AC105200 Homo sapi
386	32	12.7	59806	2	AC101192	AC101192 Mus muscu	459	32	12.7	71979	2	AC101186	AC101186 Mus muscu
387	32	12.7	60211	2	AC068685	AC068685 Homo sapi	C 460	32	12.7	72005	2	AC067776	AC067776 Homo sapi
388	32	12.7	61143	2	AC099802	AC099802 Homo sapi	C 461	32	12.7	72757	2	AC025301	AC025301 Homo sapi
389	32	12.7	61325	2	AC100109	AC100109 Mus muscu	462	32	12.7	72784	2	AC100279	AC100279 Mus muscu
390	32	12.7	61451	2	AC101514	AC101514 Mus muscu	C 463	32	12.7	73322	2	AC069380	AC069380 Homo sapi
391	32	12.7	61469	2	AC107910	AC107910 Homo sapi	C 464	32	12.7	73472	2	AC084770	AC084770 Homo sapi
c 392	32	12.7	61956	2	AC101376	AC101376 Mus muscu	C 465	32	12.7	73516	2	AC100369	AC100369 Mus muscu
393	32	12.7	62125	2	AC137958	AC137958 Mus muscu	466	32	12.7	73539	2	AC129493	AC129493 Homo sapi
c 394	32	12.7	62186	2	AC110604	AC110604 Homo sapi	C 467	32	12.7	73555	2	AC021278	AC021278 Homo sapi
c 395	32	12.7	62512	2	AC103999	AC103999 Homo sapi	468	32	12.7	73638	2	AC015613	AC015613 Homo sapi
396	32	12.7	62859	2	AC101719	AC101719 Mus muscu	C 469	32	12.7	73789	2	AC101587	AC101587 Mus muscu
397	32	12.7	62861	2	AC137726	AC137726 Homo sapi	C 470	32	12.7	74206	2	AC100080	AC100080 Mus muscu
398	32	12.7	63063	2	AC099996	AC099996 Mus muscu	C 471	32	12.7	75035	2	AC069096	AC069096 Homo sapi
399	32	12.7	63369	2	AC010861	AC010861 Homo sapi	472	32	12.7	75326	2	AC026999	AC026999 Homo sapi
400	32	12.7	63599	2	AC116159	AC116159 Homo sapi	473	32	12.7	75594	2	AC021273	AC021273 Homo sapi
c 401	32	12.7	63753	2	AC090089	AC090089 Homo sapi	C 474	32	12.7	76089	2	AC026945	AC026945 Homo sapi
c 402	32	12.7	63910	2	AC135341	AC135341 Homo sapi	C 475	32	12.7	76410	2	AC016093	AC016093 Homo sapi
403	32	12.7	63966	2	AC083929	AC083929 Homo sapi	476	32	12.7	76442	2	AC138234	AC138234 Mus muscu
404	32	12.7	64303	2	AC103754	AC103754 Homo sapi	477	32	12.7	76656	2	AC142858_3	Continuation (4 of
405	32	12.7	64439	2	AC120872	AC120872 Mus muscu	478	32	12.7	77096	2	AC016283	AC016283 Homo sapi
406	32	12.7	64536	2	AC135067	AC135067 Homo sapi	479	32	12.7	78011	2	AC016362	AC016362 Homo sapi
407	32	12.7	64611	2	AC115702	AC115702 Mus muscu	480	32	12.7	78767	2	AC100635	AC100635 Mus muscu
c 408	32	12.7	64676	2	AC136335	AC136335 Homo sapi	481	32	12.7	79938	2	AC025399	AC025399 Homo sapi
409	32	12.7	64803	2	AC091149	AC091149 Homo sapi	C 482	32	12.7	80053	2	AC022617	AC022617 Homo sapi
410	32	12.7	64869	2	AC125429	AC125429 Homo sapi	C 483	32	12.7	80318	2	AC016300	AC016300 Homo sapi
411	32	12.7	64962	2	AC124644	AC124644 Mus muscu	484	32	12.7	80866	2	AC012649	AC012649 Drosophil
412	32	12.7	65031	2	AC114338	AC114338 Mus muscu	485	32	12.7	80909	2	AC016842	AC016842 Homo sapi
c 413	32	12.7	65128	2	AC104210	AC104210 Homo sapi	486	32	12.7	81436	2	AC023552	AC023552 Homo sapi
414	32	12.7	65273	2	AC120357	AC120357 Mus muscu	C 487	32	12.7	81448	2	AC026630	AC026630 Homo sapi
415	32	12.7	65459	2	AC100135	AC100135 Mus muscu	488	32	12.7	81675	2	AC016354	AC016354 Homo sapi
c 416	32	12.7	65512	2	AC101322	AC101322 Mus muscu	489	32	12.7	82023	2	AC100643	AC100643 Mus muscu
c 417	32	12.7	65550	2	AC011923	AC011923 Homo sapi	490	32	12.7	82356	2	AC144912	AC144912 Mus muscu
418	32	12.7	65767	2	AC015704	AC015704 Homo sapi	C 491	32	12.7	82665	2	AC023204	AC023204 Homo sapi
c 419	32	12.7	65973	2	AC102332	AC102332 Mus muscu	492	32	12.7	82837	2	AC022590	AC022590 Homo sapi
c 420	32	12.7	66137	2	AC101526	AC101526 Mus muscu	C 493	32	12.7	84483	2	AC021936	AC021936 Homo sapi
c 421	32	12.7	66308	2	AC100618	AC100618 Mus muscu	C 494	32	12.7	84581	2	AC024546	AC024546 Homo sapi
422	32	12.7	66393	2	AC100424	AC100424 Mus muscu	C 495	32	12.7	85012	2	AC133713	AC133713 Rattus no
c 423	32	12.7	66639	2	AC068932	AC068932 Homo sapi	C 496	32	12.7	85049	2	AC137945	AC137945 Mus muscu
c 424	32	12.7	66686	2	AC087669	AC087669 Homo sapi	497	32	12.7	86455	2	AC126295_4	Continuation (5 of
c 425	32	12.7	66985	2	AC127516	AC127516 Homo sapi	C 498	32	12.7	87141	2	AC020662	AC020662 Homo sapi
426	32	12.7	67179	2	AC083972	AC083972 Homo sapi	499	32	12.7	87147	2	AC107496_4	Continuation (5 of
c 427	32	12.7	67224	2	AC129953	AC129953 Bos tauru	C 500	32	12.7	88940	2	AC138602	AC138602 Mus muscu
428	32	12.7	67711	2	AC090353	AC090353 Homo sapi	C 501	32	12.7	90597	2	AC142520	AC142520 Rattus no
429	32	12.7	67713	2	AC102796	AC102796 Homo sapi	C 502	32	12.7	92141	2	AC021565	AC021565 Homo sapi
c 430	32	12.7	67763	2	AC103752	AC103752 Homo sapi	C 503	32	12.7	92315	2	AC101653	AC101653 Mus muscu

504	32	12.7	92636	2	AC022747	AC022747 Homo sapi
c 505	32	12.7	93121	2	DMBR48A1	AL121844 Drosophil
c 506	32	12.7	95208	2	AC115769	AC115769 Mus muscu
507	32	12.7	95271	2	AL450383	AL450383 Homo sapi
c 508	32	12.7	95689	2	AC117735	AC117735 Mus muscu
509	32	12.7	95751	2	AC119650_3	Continuation (4 of
c 510	32	12.7	96798	2	AC138698	AC138698 Homo sapi
511	32	12.7	96895	2	AC141768	AC141768 Apis mell
c 512	32	12.7	96895	2	AC141768	AC141768 Apis mell
c 513	32	12.7	97021	2	AC138255	AC138255 Mus muscu
514	32	12.7	104494	2	AC012166	AC012166 Drosophil
515	32	12.7	105011	2	AC096724	AC096724 Homo sapi
516	32	12.7	107007	2	AC142685	AC142685 Macaca mu
517	32	12.7	107304	2	AC016274	AC016274 Homo sapi
518	32	12.7	110000	2	AC009801	AC009801 Homo sapi
c 519	32	12.7	110000	2	AC091343_5	Continuation (6 of
520	32	12.7	110000	2	AC095863_08	Continuation (9 of
521	32	12.7	110000	2	AC097780_0	AC097780 Rattus no
522	32	12.7	110000	2	AC098036_1	Continuation (2 of
523	32	12.7	110000	2	AC106413_2	Continuation (3 of
c 524	32	12.7	110000	2	AC112563_3	Continuation (4 of
c 525	32	12.7	110000	2	AC115386_1	Continuation (2 of
526	32	12.7	110000	2	AC018724_0	AC018724 Homo sapi
c 527	32	12.7	110000	2	AC140288_0	AC140288 Mus muscu
528	32	12.7	110000	2	AC140288_1	Continuation (2 of
c 529	32	12.7	110000	2	AC141230_0	AC141230 Homo sapi
530	32	12.7	110000	2	AC142976_0	AC142976 Macaca mu
c 531	32	12.7	110000	2	AL831785_5	Continuation (6 of
532	32	12.7	110000	2	AL831785_7	Continuation (8 of
533	32	12.7	110000	2	AL929091_12	Continuation (13 o
c 534	32	12.7	117710	2	AC111053	AC111053 Mus muscu
535	32	12.7	120316	2	AC025984	AC025984 Homo sapi
c 536	32	12.7	125150	2	AC005450	AC005450 Drosophil
537	32	12.7	127362	2	AC010014	AC010014 Drosophil
c 538	32	12.7	127372	2	AC068172	AC068172 Mus muscu
c 539	32	12.7	127373	2	AC013330	AC013330 Homo sapi
540	32	12.7	127505	2	AC061980	AC061980 Homo sapi
c 541	32	12.7	128465	2	AC138569	AC138569 Gallus ga
c 542	32	12.7	128561	2	AC068729	AC068729 Homo sapi
543	32	12.7	128822	2	AP001260	AP001260 Homo sapi
c 544	32	12.7	129218	2	AC138851	AC138851 Homo sapi
545	32	12.7	129451	2	AC073783	AC073783 Mus muscu
546	32	12.7	129755	2	AC019296	AC019296 Homo sapi
c 547	32	12.7	131298	2	AC142959	AC142959 Macaca mu
c 548	32	12.7	131694	2	AC009619	AC009619 Homo sapi
c 549	32	12.7	132270	2	AC141705	AC141705 Apis mell
550	32	12.7	132290	2	AC026137	AC026137 Homo sapi
c 551	32	12.7	133273	2	AC068586	AC068586 Homo sapi
c 552	32	12.7	133622	2	AC141813	AC141813 Apis mell
553	32	12.7	133997	2	AC015469	AC015469 Homo sapi
554	32	12.7	134940	2	AC018939	AC018939 Homo sapi
c 555	32	12.7	135321	2	AC142021	AC142021 Rattus no
556	32	12.7	136212	2	AC139386	AC139386 Rattus no
557	32	12.7	136448	2	AC012231	AC012231 Homo sapi
c 558	32	12.7	136869	2	AP005193	AP005193 Oryza sat
c 559	32	12.7	137911	2	AC009769	AC009769 Homo sapi
c 560	32	12.7	138295	2	AC024448	AC024448 Homo sapi
c 561	32	12.7	140897	2	AC143170	AC143170 Macaca mu
562	32	12.7	141529	2	AC025330	AC025330 Homo sapi
c 563	32	12.7	142126	2	AC026139	AC026139 Homo sapi
c 564	32	12.7	142781	2	AC141934	AC141934 Rattus no
565	32	12.7	142986	2	AC023467	AC023467 Homo sapi
566	32	12.7	143409	2	AP001787	AP001787 Homo sapi
567	32	12.7	144888	2	AC023895	AC023895 Homo sapi
568	32	12.7	146814	2	AC022320	AC022320 Homo sapi
c 569	32	12.7	149269	2	AC008690	AC008690 Homo sapi
c 570	32	12.7	150207	2	AL451067	AL451067 Homo sapi
c 571	32	12.7	150477	2	AC024441	AC024441 Homo sapi
572	32	12.7	152141	2	AC090189	AC090189 Homo sapi
c 573	32	12.7	152575	2	AC141690	AC141690 Apis mell
574	32	12.7	153469	2	AC130528	AC130528 Mus muscu
575	32	12.7	153833	2	AP001996	AP001996 Homo sapi
c 576	32	12.7	157953	2	AC141134	AC141134 Rattus no

32	12.7	158229	2	AC021363	AC021363 Homo sapi
32	12.7	159299	2	AC114713	AC114713 Rattus no
32	12.7	159670	2	AC140157	AC140157 Canis fam
32	12.7	160699	2	AC138731	AC138731 Pongo pyg
32	12.7	160737	2	AC026213	AC026213 Homo sapi
32	12.7	162493	2	AC073972	AC073972 Homo sapi
32	12.7	162508	2	AC025870	AC025870 Homo sapi
32	12.7	162606	2	AC016348	AC016348 Homo sapi
32	12.7	163551	2	AC015777	AC015777 Homo sapi
32	12.7	163916	2	AP002413	AP002413 Homo sapi
32	12.7	164159	2	AC100853	AC100853 Homo sapi
32	12.7	164297	2	AC012138	AC012138 Homo sapi
32	12.7	164396	2	AC024961	AC024961 Homo sapi
32	12.7	164473	2	AP001108	AP001108 Homo sapi
32	12.7	164652	2	AC026923	AC026923 Homo sapi
32	12.7	164846	2	AC023007	AC023007 Homo sapi
32	12.7	164918	2	AC013373	AC013373 Homo sapi
32	12.7	165278	2	AC087823	AC087823 Homo sapi
32	12.7	165404	2	AC084119	AC084119 Homo sapi
32	12.7	166549	2	AC025990	AC025990 Homo sapi
32	12.7	166689	2	AC058815	AC058815 Homo sapi
32	12.7	167305	2	AL590409	AL590409 Homo sapi
32	12.7	167833	2	AC122742	AC122742 Mus muscu
32	12.7	168081	2	AC083955	AC083955 Mus muscu
32	12.7	168262	2	AC143997	AC143997 Macaca mu
32	12.7	168527	2	AC040993	AC040993 Homo sapi
32	12.7	169328	2	AC016281	AC016281 Homo sapi
32	12.7	169457	2	AC009216	AC009216 Drosophil
32	12.7	170393	2	AC024304	AC024304 Homo sapi
32	12.7	170496	2	AC137002	AC137002 Oryza sat
32	12.7	170795	2	AC021346	AC021346 Homo sapi
32	12.7	172346	2	AC016349	AC016349 Homo sapi
32	12.7	172387	2	AC103561	AC103561 Homo sapi
32	12.7	172485	2	AC141978	AC141978 Rattus no
32	12.7	172562	2	AC136120	AC136120 Rattus no
32	12.7	173340	2	AC015760	AC015760 Homo sapi
32	12.7	173917	2	AC027476	AC027476 Homo sapi
32	12.7	174280	2	AL356116	AL356116 Homo sapi
32	12.7	174393	2	AC126618	AC126618 Rattus no
32	12.7	174815	2	AP001390	AP001390 Homo sapi
32	12.7	174937	2	AC022245	AC022245 Homo sapi
32	12.7	175260	2	AC119361	AC119361 Rattus no
32	12.7	175288	2	AC023589	AC023589 Homo sapi
32	12.7	175771	2	AC016510	AC016510 Homo sapi
32	12.7	175807	2	AC101863	AC101863 Mus muscu
32	12.7	175977	2	AC058808	AC058808 Homo sapi
32	12.7	176372	2	AC026030	AC026030 Homo sapi
32	12.7	177531	2	AC129120	AC129120 Rattus no
32	12.7	177635	2	AC141509	AC141509 Rattus no
32	12.7	177680	2	AP001910	AP001910 Homo sapi
32	12.7	178122	2	AC095848	AC095848 Rattus no
32	12.7	178384	2	AL591026	AL591026 Homo sapi
32	12.7	178640	2	AC069170	AC069170 Homo sapi
32	12.7	179323	2	AC011852	AC011852 Homo sapi
32	12.7	179845	2	AY178787	AY178787 Canis fam
32	12.7	180018	2	AC023417	AC023417 Homo sapi
32	12.7	180044	2	AC026942	AC026942 Homo sapi
32	12.7	181290	2	BX005286	BX005286 Danio rer
32	12.7	182673	2	AC073105	AC073105 Homo sapi
32	12.7	182690	2	AC009998	AC009998 Homo sapi
32	12.7	182799	2	AC073526	AC073526 Homo sapi
32	12.7	182990	2	AC125866	AC125866 Rattus no
32	12.7	183345	2	AC120550	AC120550 Mus muscu
32	12.7	183350	2	AC102305	AC102305 Mus muscu
32	12.7	184127	2	AC140578	AC140578 Macaca mu
32	12.7	184244	2	AC073282	AC073282 Homo sapi
32	12.7	184767	2	AC127990	AC127990 Rattus no
32	12.7	185272	2	AC084363	AC084363 Homo sapi
32	12.7	185272	2	AC121394	AC121394 Rattus no
32	12.7	185360	2	AC126230	AC126230 Bos tauru
32	12.7	185440	2	AC015499	AC015499 Homo sapi
32	12.7	185810	2	AC136052	AC136052 Rattus no



C 650	32	12.7 186044	2	AC084099	AC084099 Homo sapi	723	32	12.7 229916	2	AC132022	AC132022 Rattus no
651	32	12.7 186184	2	AC139894	AC139894 Rattus no	724	32	12.7 230254	2	AC074163	AC074163 Mus muscu
652	32	12.7 187038	2	AC021179	AC021179 Homo sapi	725	32	12.7 230273	2	AC110400	AC110400 Rattus no
C 653	32	12.7 187150	2	AC016282	AC016282 Homo sapi	C 726	32	12.7 230393	2	AC133303	AC133303 Rattus no
C 654	32	12.7 187557	2	AC074223	AC074223 Mus muscu	C 727	32	12.7 230787	2	AC103473	AC103473 Rattus no
C 655	32	12.7 188152	2	AC025847	AC025847 Homo sapi	728	32	12.7 230877	2	AC105583	AC105583 Rattus no
656	32	12.7 188540	2	AC011108	AC011108 Homo sapi	729	32	12.7 231772	2	AC124926	AC124926 Rattus no
C 657	32	12.7 191109	2	AC137370	AC137370 Rattus no	730	32	12.7 232244	2	AC114524	AC114524 Rattus no
C 658	32	12.7 192142	2	AC136061	AC136061 Rattus no	731	32	12.7 232792	2	AC106657	AC106657 Rattus no
C 659	32	12.7 192372	2	AC134754	AC134754 Rattus no	C 732	32	12.7 233247	2	AC134936	AC134936 Rattus no
C 660	32	12.7 193001	2	AC023231	AC023231 Homo sapi	733	32	12.7 233363	2	AC078919	AC078919 Homo sapi
661	32	12.7 194069	2	AC128533	AC128533 Rattus no	C 734	32	12.7 233980	2	AC133857	AC133857 Rattus no
662	32	12.7 194247	2	AC128060	AC128060 Rattus no	C 735	32	12.7 234213	2	BX510954	BX510954 Danio rer
663	32	12.7 194328	2	AC139902	AC139902 Rattus no	C 736	32	12.7 235554	2	AC118332	AC118332 Rattus no
664	32	12.7 195506	2	AC015796	AC015796 Mus muscu	C 737	32	12.7 235662	2	AC126709	AC126709 Rattus no
665	32	12.7 195637	2	AP002420	AP002420 Homo sapi	C 738	32	12.7 235877	2	AC117278	AC117278 Rattus no
C 666	32	12.7 196083	2	AC027092	AC027092 Homo sapi	739	32	12.7 235918	2	AC127741	AC127741 Rattus no
C 667	32	12.7 196119	2	AP001799	AP001799 Homo sapi	C 740	32	12.7 235933	2	AC097843	AC097843 Rattus no
C 668	32	12.7 196146	2	AC023609	AC023609 Mus muscu	C 741	32	12.7 236303	2	AC102981	AC102981 Rattus no
669	32	12.7 196990	2	AC134013	AC134013 Rattus no	C 742	32	12.7 236402	2	AC120673	AC120673 Rattus no
670	32	12.7 198248	2	AP001487	AP001487 Homo sapi	C 743	32	12.7 236527	2	AC134501	AC134501 Rattus no
671	32	12.7 198782	2	AC144252	AC144252 Macaca mu	744	32	12.7 236550	2	AC111801	AC111801 Rattus no
672	32	12.7 199263	2	BX004992	BX004992 Danio rer	C 745	32	12.7 236957	2	AC118153	AC118153 Rattus no
C 673	32	12.7 199301	2	BX088589	BX088589 Danio rer	C 746	32	12.7 237192	2	AC013375	AC013375 Homo sapi
674	32	12.7 199733	2	AC107682	AC107682 Mus muscu	747	32	12.7 237838	2	AC121282	AC121282 Mus muscu
675	32	12.7 200000	2	AC008076	AC008076 Homo sapi	748	32	12.7 238285	2	AC109573	AC109573 Rattus no
676	32	12.7 201094	2	AC020995	AC020995 Homo sapi	749	32	12.7 238839	2	AC123162	AC123162 Rattus no
C 677	32	12.7 201929	2	AC126087	AC126087 Rattus no	C 750	32	12.7 239398	2	AC105708	AC105708 Rattus no
C 678	32	12.7 202033	2	BX511251	BX511251 Danio rer	C 751	32	12.7 239851	2	AC101712	AC101712 Mus muscu
C 679	32	12.7 202878	2	AC137548	AC137548 Macaca mu	752	32	12.7 239880	2	AC095415	AC095415 Rattus no
C 680	32	12.7 204990	2	AC138163	AC138163 Bos tauru	753	32	12.7 239915	2	AC097168	AC097168 Rattus no
C 681	32	12.7 205158	2	AC015703	AC015703 Homo sapi	C 754	32	12.7 239986	2	AC097238	AC097238 Rattus no
C 682	32	12.7 206159	2	AC107737	AC107737 Mus muscu	755	32	12.7 240561	2	AC108554	AC108554 Rattus no
C 683	32	12.7 207193	2	AC137471	AC137471 Rattus no	756	32	12.7 241109	2	AC106232	AC106232 Rattus no
C 684	32	12.7 207588	2	AC087162	AC087162 Mus muscu	757	32	12.7 241587	2	AC096197	AC096197 Rattus no
C 685	32	12.7 208180	2	AC116722	AC116722 Mus muscu	758	32	12.7 241725	2	AC112295	AC112295 Rattus no
686	32	12.7 208936	2	AC141215	AC141215 Rattus no	C 759	32	12.7 241865	2	AC118396	AC118396 Rattus no
687	32	12.7 210752	2	AC098606	AC098606 Rattus no	C 760	32	12.7 242882	2	AC094356	AC094356 Rattus no
C 688	32	12.7 211341	2	AC103309	AC103309 Rattus no	C 761	32	12.7 243739	2	AC095239	AC095239 Rattus no
C 689	32	12.7 211375	2	AC141149	AC141149 Rattus no	C 762	32	12.7 243789	2	AC136416	AC136416 Rattus no
C 690	32	12.7 211973	2	AP001163	AP001163 Homo sapi	C 763	32	12.7 243884	2	AC130044	AC130044 Rattus no
691	32	12.7 213514	2	AC079500	AC079500 Mus muscu	C 764	32	12.7 244389	2	AC111858	AC111858 Rattus no
692	32	12.7 213947	2	AC135988	AC135988 Homo sapi	765	32	12.7 245394	2	AC125756	AC125756 Rattus no
693	32	12.7 214767	2	AC103390	AC103390 Mus muscu	766	32	12.7 245892	2	AC107095	AC107095 Rattus no
C 694	32	12.7 215495	2	AC121649	AC121649 Rattus no	C 767	32	12.7 246337	2	AC106464	AC106464 Rattus no
C 695	32	12.7 215541	2	AC016904	AC016904 Homo sapi	C 768	32	12.7 246387	2	AC109737	AC109737 Rattus no
696	32	12.7 217028	2	AC140694	AC140694 Rattus no	C 769	32	12.7 246710	2	AC094240	AC094240 Rattus no
C 697	32	12.7 217336	2	AC131344	AC131344 Rattus no	C 770	32	12.7 247017	2	AC105601	AC105601 Rattus no
C 698	32	12.7 217822	2	AC131135	AC131135 Rattus no	771	32	12.7 247659	2	AC095548	AC095548 Rattus no
699	32	12.7 219752	2	AC115297	AC115297 Mus muscu	C 772	32	12.7 248449	2	AC137398	AC137398 Rattus no
C 700	32	12.7 219949	2	AC105796	AC105796 Rattus no	773	32	12.7 248664	2	AC133854	AC133854 Rattus no
701	32	12.7 221260	2	AC122444	AC122444 Mus muscu	774	32	12.7 248682	2	AC095449	AC095449 Rattus no
C 702	32	12.7 221962	2	AC136580	AC136580 Rattus no	C 775	32	12.7 248720	2	AC114351	AC114351 Rattus no
C 703	32	12.7 222072	2	AC141069	AC141069 Homo sapi	C 776	32	12.7 249131	2	AC121717	AC121717 Rattus no
704	32	12.7 223090	2	AC111554	AC111554 Rattus no	777	32	12.7 250683	2	AC115272	AC115272 Rattus no
705	32	12.7 223225	2	AC112468	AC112468 Rattus no	778	32	12.7 251703	2	AC114450	AC114450 Rattus no
706	32	12.7 223687	2	AC121373	AC121373 Rattus no	779	32	12.7 252215	2	AC137271	AC137271 Rattus no
C 707	32	12.7 223875	2	AC133941	AC133941 Mus muscu	C 780	32	12.7 252715	2	AC127819	AC127819 Rattus no
708	32	12.7 224031	2	AC137234	AC137234 Rattus no	781	32	12.7 252925	2	AC021048	AC021048 Homo sapi
C 709	32	12.7 224726	2	AC097428	AC097428 Rattus no	782	32	12.7 253067	2	AC142237	AC142237 Rattus no
C 710	32	12.7 224758	2	AC128387	AC128387 Rattus no	783	32	12.7 253752	2	AC109934	AC109934 Rattus no
C 711	32	12.7 225154	2	AC106152	AC106152 Rattus no	C 784	32	12.7 254217	2	AC114075	AC114075 Rattus no
C 712	32	12.7 225773	2	AC114232	AC114232 Rattus no	785	32	12.7 254668	2	AC109742	AC109742 Rattus no
C 713	32	12.7 226077	2	AC013296	AC013296 Homo sapi	C 786	32	12.7 254721	2	AC120733	AC120733 Rattus no
714	32	12.7 226135	2	AC110712	AC110712 Rattus no	C 787	32	12.7 255032	2	AC107178	AC107178 Rattus no
715	32	12.7 227224	2	AC094832	AC094832 Rattus no	C 788	32	12.7 255641	2	AC096524	AC096524 Rattus no
716	32	12.7 227767	2	AC118766	AC118766 Rattus no	C 789	32	12.7 255713	2	AC099293	AC099293 Rattus no
717	32	12.7 227827	2	AC131809	AC131809 Rattus no	C 790	32	12.7 256290	2	AC098754	AC098754 Rattus no
C 718	32	12.7 228052	2	AC094440	AC094440 Rattus no	C 791	32	12.7 256348	2	AC095686	AC095686 Rattus no
C 719	32	12.7 228653	2	AC098441	AC098441 Rattus no	792	32	12.7 256433	2	AC101703	AC101703 Mus muscu
720	32	12.7 229506	2	AL161933	AL161933 Homo sapi	C 793	32	12.7 256643	2	AC122567	AC122567 Rattus no
C 721	32	12.7 229701	2	AC140109	AC140109 Mus muscu	C 794	32	12.7 257444	2	AC099424	AC099424 Rattus no
722	32	12.7 229849	2	AC128399	AC128399 Rattus no	C 795	32	12.7 257677	2	AC095819	AC095819 Rattus no

C 796	32	12.7	257679	2	AC134801	AC134801 Rattus no	869	31	12.4	20674	2	AC136474	AC136474 Homo sapi
C 797	32	12.7	258303	2	AC095938	AC095938 Rattus no	C 870	31	12.4	20712	2	AC013425	AC013425 Drosophil
C 798	32	12.7	258593	2	AC108965	AC108965 Rattus no	C 871	31	12.4	23788	2	AC068201	AC068201 Homo sapi
C 799	32	12.7	259631	2	AC095168	AC095168 Rattus no	C 872	31	12.4	27709	2	LMFLCHR32_27	Continuation (28 o
C 800	32	12.7	259694	2	AC139848	AC139848 Mus muscu	C 873	31	12.4	29590	2	AC015588	AC015588 Homo sapi
C 801	32	12.7	260017	2	AC098371	AC098371 Rattus no	C 874	31	12.4	29590	2	AC015588	AC015588 Homo sapi
C 802	32	12.7	260024	2	AC095715	AC095715 Rattus no	C 875	31	12.4	30237	2	AC115096	AC115096 Homo sapi
C 803	32	12.7	260573	2	AC125775	AC125775 Rattus no	C 876	31	12.4	30758	2	CEH05104	Z94122 Caenorhabdi
C 804	32	12.7	260805	2	AC097233	AC097233 Rattus no	C 877	31	12.4	32421	2	CEH25F02	Z93633 Caenorhabdi
C 805	32	12.7	261061	2	AC127435	AC127435 Rattus no	C 878	31	12.4	34145	2	AC079312	AC079312 Homo sapi
C 806	32	12.7	261604	2	AC119819	AC119819 Mus muscu	C 879	31	12.4	34886	2	AC133621	AC133621 Rattus no
C 807	32	12.7	261825	2	AC106351	AC106351 Rattus no	C 880	31	12.4	35195	2	AC068589	AC068589 Homo sapi
C 808	32	12.7	262061	2	AC117172	AC117172 Rattus no	C 881	31	12.4	36102	2	AC101082	AC101082 Mus muscu
C 809	32	12.7	262386	2	AC126101	AC126101 Rattus no	C 882	31	12.4	36546	2	AC100555	AC100555 Mus muscu
C 810	32	12.7	262984	2	AC095212	AC095212 Rattus no	C 883	31	12.4	37887	2	AC068453	AC068453 Homo sapi
C 811	32	12.7	265985	2	AC087226	AC087226 Mus muscu	C 884	31	12.4	38271	2	AC100969	AC100969 Mus muscu
C 812	32	12.7	267188	2	AC135827	AC135827 Rattus no	C 885	31	12.4	38824	2	AC087716	AC087716 Homo sapi
C 813	32	12.7	268279	2	AC097205	AC097205 Rattus no	C 886	31	12.4	39049	2	AC137692	AC137692 Mus muscu
C 814	32	12.7	272675	2	AC114467	AC114467 Rattus no	C 887	31	12.4	39186	2	AC136757	AC136757 Homo sapi
C 815	32	12.7	275351	2	AC117883	AC117883 Rattus no	C 888	31	12.4	40125	2	AC132818	AC132818 Homo sapi
C 816	32	12.7	276168	2	AC105518	AC105518 Rattus no	C 889	31	12.4	40764	2	AC126382	AC126382 Homo sapi
C 817	32	12.7	279112	2	AC132048	AC132048 Rattus no	C 890	31	12.4	41132	2	AC022741	AC022741 Homo sapi
C 818	32	12.7	279233	2	AC132167	AC132167 Rattus no	C 891	31	12.4	41356	2	AC069190	AC069190 Homo sapi
C 819	32	12.7	279587	2	AC112408	AC112408 Rattus no	C 892	31	12.4	41398	2	AC104853	AC104853 Homo sapi
C 820	32	12.7	284442	2	AC107002	AC107002 Rattus no	C 893	31	12.4	41399	2	AC129587	AC129587 Mus muscu
C 821	32	12.7	287080	2	AC096696	AC096696 Rattus no	C 894	31	12.4	42029	2	AC114762	AC114762 Homo sapi
C 822	32	12.7	290179	2	AC134072	AC134072 Rattus no	C 895	31	12.4	42170	2	AC104252	AC104252 Homo sapi
C 823	32	12.7	290633	2	AC099180	AC099180 Rattus no	C 896	31	12.4	42293	2	AC023531	AC023531 Homo sapi
C 824	32	12.7	291205	2	AC103125	AC103125 Rattus no	C 897	31	12.4	42614	2	AC127805_4	Continuation (5 of
C 825	32	12.7	293507	2	AC097292	AC097292 Rattus no	C 898	31	12.4	42818	2	AC013249	AC013249 Homo sapi
C 826	32	12.7	295708	2	AC102357	AC102357 Mus muscu	C 899	31	12.4	43295	2	AC024381	AC024381 Homo sapi
C 827	32	12.7	298503	2	AC102645	AC102645 Mus muscu	C 900	31	12.4	44005	2	AC104755	AC104755 Homo sapi
C 828	32	12.7	298532	2	AC129468	AC129468 Rattus no	C 901	31	12.4	46069	2	AC133288	AC133288 Homo sapi
C 829	32	12.7	305911	2	AC115447	AC115447 Rattus no	C 902	31	12.4	46397	2	AC134159	AC134159 Rattus no
C 830	32	12.7	306103	2	AC127202	AC127202 Rattus no	C 903	31	12.4	46405	2	AC027255	AC027255 Homo sapi
C 831	32	12.7	309771	2	AC117311	AC117311 Rattus no	C 904	31	12.4	46595	2	AC101015	AC101015 Mus muscu
C 832	32	12.7	314959	2	AC106099	AC106099 Rattus no	C 905	31	12.4	46742	2	AC100281	AC100281 Mus muscu
C 833	32	12.7	318620	2	AC110910	AC110910 Mus muscu	C 906	31	12.4	46889	2	AC091081	AC091081 Homo sapi
C 834	32	12.7	321777	2	AC118532	AC118532 Rattus no	C 907	31	12.4	47269	2	AC068834	AC068834 Homo sapi
C 835	32	12.7	322361	2	AC139220	AC139220 Mus muscu	C 908	31	12.4	47417	2	AC100702	AC100702 Mus muscu
C 836	32	12.7	326209	2	AC134065	AC134065 Rattus no	C 909	31	12.4	47425	2	AC009934	AC009934 Homo sapi
C 837	32	12.7	326739	2	AC142901	AC142901 Macaca mu	C 910	31	12.4	47533	2	AC101284	AC101284 Mus muscu
C 838	32	12.7	331675	2	AC097919	AC097919 Rattus no	C 911	31	12.4	47768	2	AC109310	AC109310 Homo sapi
C 839	32	12.7	337720	2	AC121050	AC121050 Rattus no	C 912	31	12.4	48460	2	AC101029	AC101029 Mus muscu
C 840	32	12.7	338453	2	AC112044	AC112044 Rattus no	C 913	31	12.4	48606	2	AC025671	AC025671 Homo sapi
C 841	32	12.7	342586	2	AC109682	AC109682 Rattus no	C 914	31	12.4	49397	2	AC087640	AC087640 Homo sapi
C 842	32	12.7	343504	2	AL158031	AL158031 Homo sapi	C 915	31	12.4	49580	2	AC136347	AC136347 Homo sapi
C 843	31	12.4	121	11	G42786	G42786 BSM66 Plasm	C 916	31	12.4	49976	2	AC025670	AC025670 Homo sapi
C 844	31	12.4	409	6	AX677607	AX677607 Sequence	C 917	31	12.4	50139	2	AC068883	AC068883 Homo sapi
C 845	31	12.4	513	3	AY175837	AY175837 Laupala k	C 918	31	12.4	50215	2	AC060819	AC060819 Homo sapi
C 846	31	12.4	513	3	AY175840	AY175840 Laupala h	C 919	31	12.4	50215	2	AC060819	AC060819 Homo sapi
C 847	31	12.4	736	8	AY216600	AY216600 Juncus pa	C 920	31	12.4	50411	2	AC087304	AC087304 Homo sapi
C 848	31	12.4	1075	6	AR231970	AR231970 Sequence	C 921	31	12.4	50487	2	AC068211	AC068211 Homo sapi
C 849	31	12.4	1075	6	BD135520	BD135520 Neurotrop	C 922	31	12.4	50905	2	AC099853	AC099853 Mus muscu
C 850	31	12.4	1076	6	AR231986	AR231986 Sequence	C 923	31	12.4	51234	2	AC102920	AC102920 Mus muscu
C 851	31	12.4	1214	8	PSWRR18S	L16011 Pseudowinte	C 924	31	12.4	51275	2	AC090351	AC090351 Homo sapi
C 852	31	12.4	1402	8	AF146215	AF146215 Mazzaella	C 925	31	12.4	51340	2	AC025213	AC025213 Homo sapi
C 853	31	12.4	1428	8	AAZ97639	Z97639 Acantholimo	C 926	31	12.4	51381	2	AC136770	AC136770 Homo sapi
C 854	31	12.4	1462	8	AF284902	AF284902 Carex dig	C 927	31	12.4	51754	2	AC129479	AC129479 Mus muscu
C 855	31	12.4	1471	8	AF284899	AF284899 Carex lim	C 928	31	12.4	51883	2	AC135993	AC135993 Homo sapi
C 856	31	12.4	1494	8	AF284907	AF284907 Carex lan	C 929	31	12.4	52302	2	AC099867	AC099867 Mus muscu
C 857	31	12.4	1560	6	AX512749	AX512749 Sequence	C 930	31	12.4	52614	2	AC090899	AC090899 Mus muscu
C 858	31	12.4	1666	8	AF284916	AF284916 Carex mac	C 931	31	12.4	52783	2	AC100403	AC100403 Mus muscu
C 859	31	12.4	1675	8	AF284900	AF284900 Carex ova	C 932	31	12.4	52806	2	AC090158	AC090158 Homo sapi
C 860	31	12.4	2157	6	AR231967	AR231967 Sequence	C 933	31	12.4	53121	2	AC136331	AC136331 Homo sapi
C 861	31	12.4	2157	6	BD135517	BD135517 Neurotrop	C 934	31	12.4	53435	2	AC135259	AC135259 Homo sapi
C 862	31	12.4	2158	6	AR231983	AR231983 Sequence	C 935	31	12.4	53439	2	AC140621	AC140621 Macaca mu
C 863	31	12.4	2568	6	AR231959	AR231959 Sequence	C 936	31	12.4	53581	2	AC120351	AC120351 Mus muscu
C 864	31	12.4	2568	6	BD135509	BD135509 Neurotrop	C 937	31	12.4	53659	2	AC013255	AC013255 Drosophil
C 865	31	12.4	3209	6	AR231961	AR231961 Sequence	C 938	31	12.4	53871	2	AC132821	AC132821 Homo sapi
C 866	31	12.4	3209	6	AR231977	AR231977 Sequence	C 939	31	12.4	54245	2	AC100907	AC100907 Mus muscu
C 867	31	12.4	3209	6	BD135511	BD135511 Neurotrop	C 940	31	12.4	54257	2	AC100202	AC100202 Mus muscu
C 868	31	12.4	15503	2	AC125536	AC125536 Mus muscu	C 941	31	12.4	54383	2	AC100305	AC100305 Mus muscu



C 942	31	12.4	54450	2	AC080179	AC080179 Homo sapi
943	31	12.4	54452	2	AC103860	AC103860 Homo sapi
C 944	31	12.4	54612	2	AC103821	AC103821 Homo sapi
C 945	31	12.4	54706	2	AC100048	AC100048 Mus muscu
946	31	12.4	54777	2	AC1013651	AC1013651 Homo sapi
C 947	31	12.4	54958	2	AC090760	AC090760 Homo sapi
948	31	12.4	55238	2	AC013422	AC013422 Drosophil
949	31	12.4	55283	2	AC100610	AC100610 Mus muscu
C 950	31	12.4	55774	2	AC091303	AC091303 Homo sapi
C 951	31	12.4	55801	2	AC087476	AC087476 Homo sapi
952	31	12.4	55973	2	AC079107	AC079107 Homo sapi
953	31	12.4	56083	2	AC141162	AC141162 Rattus no
954	31	12.4	56133	2	AC115998	AC115998 Homo sapi
955	31	12.4	56134	2	AC132199	AC132199 Homo sapi
956	31	12.4	56328	2	AC068514	AC068514 Homo sapi
957	31	12.4	56507	2	AC055770	AC055770 Homo sapi
C 958	31	12.4	56970	2	AC138096	AC138096 Homo sapi
C 959	31	12.4	57028	2	AC131078	AC131078 Mus muscu
C 960	31	12.4	57058	2	AC069455	AC069455 Homo sapi
C 961	31	12.4	57258	2	AC130342	AC130342 Homo sapi
C 962	31	12.4	57448	2	AC013539	AC013539 Homo sapi
963	31	12.4	57591	2	AC069490	AC069490 Homo sapi
964	31	12.4	57671	2	AC124003	AC124003 Homo sapi
C 965	31	12.4	57843	2	AC110290	AC110290 Homo sapi
C 966	31	12.4	57843	2	AC136651	AC136651 Rattus no
C 967	31	12.4	57877	2	AC100077	AC100077 Mus muscu
C 968	31	12.4	58040	2	AC101628	AC101628 Mus muscu
C 969	31	12.4	58081	2	AC010841	AC010841 Drosophil
C 970	31	12.4	58090	2	AC105092	AC105092 Homo sapi
971	31	12.4	58172	2	AC083793	AC083793 Homo sapi
C 972	31	12.4	58207	2	AC136762	AC136762 Homo sapi
973	31	12.4	58261	2	AC139489_4	Continuation (5 Of
974	31	12.4	58279	2	AC104354	AC104354 Homo sapi
975	31	12.4	58329	2	AC118271	AC118271 Homo sapi
976	31	12.4	58508	2	AC100320	AC100320 Mus muscu
977	31	12.4	58560	2	AC131048	AC131048 Homo sapi
C 978	31	12.4	58603	2	AC101496	AC101496 Mus muscu
979	31	12.4	58866	2	AC090594	AC090594 Homo sapi
980	31	12.4	59006	2	AC118054	AC118054 Homo sapi
981	31	12.4	59061	2	AC090749	AC090749 Homo sapi
C 982	31	12.4	59445	2	AC090596	AC090596 Homo sapi
C 983	31	12.4	59731	2	AC067830	AC067830 Homo sapi
C 984	31	12.4	59763	2	AC137116	AC137116 Mus muscu
985	31	12.4	59770	2	AC084259	AC084259 Homo sapi
C 986	31	12.4	59915	2	AC100984	AC100984 Mus muscu
987	31	12.4	59926	2	AC107461	AC107461 Homo sapi
988	31	12.4	59928	2	AC068229	AC068229 Homo sapi
989	31	12.4	59967	2	AC073302	AC073302 Homo sapi
C 990	31	12.4	60108	2	AC090854	AC090854 Homo sapi
991	31	12.4	60190	2	AC127498	AC127498 Homo sapi
C 992	31	12.4	60265	2	AC073445	AC073445 Homo sapi
993	31	12.4	60329	2	AC091109	AC091109 Homo sapi
994	31	12.4	60456	2	AC087634	AC087634 Homo sapi
995	31	12.4	60504	2	AC090716	AC090716 Homo sapi
C 996	31	12.4	60661	2	AC024389	AC024389 Homo sapi
997	31	12.4	60814	2	AC073622	AC073622 Homo sapi
C 998	31	12.4	60958	2	AC132203	AC132203 Homo sapi
999	31	12.4	60995	2	AC096119_3	Continuation (4 Of
C1000	31	12.4	61010	2	AC087492	AC087492 Homo sapi

ALIGNMENTS

RESULT 1	AC015736	77433 bp	DNA	linear	HTG 13-JUL-2000
LOCUS	AC015736				
DEFINITION	Homo sapiens clone RP11-1D13, LOW-PASS SEQUENCE SAMPLING.				
ACCESSION	AC015736				
VERSION	AC015736.2	GI:9108790			
KEYWORDS	HTG; HTGS_PHASE0.				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 77433)  
Birren,B., Linton,L., Nusbaum,C. and Lander,E.  
Homo sapiens, clone RP11-1D13  
Unpublished  
2 (bases 1 to 77433)  
Birren,B., Linton,L., Nusbaum,C., Lander,E., Allen,N., Anderson,M., Baldwin,J., Barna,N., Beckerly,R., Boguslavkiy,L., Boukhgalter,B., Brown,A., Castle,A., Colangelo,M., Collins,S., Collamore,A., Cooke,P., DeArelano,K., Dewar,K., Domino,M., Donelan,L., Doyle,M., Ferreira,P., FitzHugh,W., Forrest,C., Funke,R., Gage,D., Galagan,J., Gardyna,S., Grant,G., Hagos,B., Heaford,A., Horton,L., Howland,J.C., Johnson,R., Jones,C., Kann,L., Karatas,A., Klein,J., Lehoczyk,J., Lieu,C., Locke,K., Macdonald,P., Marquis,N., McEwan,P., McGurk,A., McKernan,K., McLaughlin,J., Meldrim,J., Morrow,J., Naylor,J., Norman,C.H., O'Connor,T., O'Donnell,P., Peterson,K., Pollara,V., Riley,R., Roy,A., Santos,R., Severy,P., Stange-Thomann,N., Stojanovic,N., Subramanian,A., Talamas,J., Tesfaye,S., Tirrell,A., Vassiliev,H., Vo,A., Wheeler,J., Wu,X., Wyman,D., Ye,W.J., Zimmer,A. and Zody,M.  
Direct Submission  
Submitted (17-NOV-1999) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA  
On Jul 13, 2000 this sequence version replaced gi:6446951.  
All repeats were identified using RepeatMasker:  
Smit, A.F.A. & Green, P. (1996-1997)  
http://ftp.genome.washington.edu/RM/RepeatMasker.html  
----- Genome Center  
Center: Whitehead Institute/ MIT Center for Genome Research  
Center code: WIBR  
Web site: http://www-seq.wi.mit.edu  
Contact: sequence\_submissions@genome.wi.mit.edu  
----- Project Information  
Center project name: L1436  
Center clone name: 1\_D\_13  
-----

TITLE  
JOURNAL  
COMMENT

\* NOTE: This record contains 76 individual  
\* sequencing reads that have not been assembled into  
\* contigs. Runs of N are used to separate the reads  
\* and the order in which they appear is completely  
\* arbitrary. Low-pass sequence sampling is useful for  
\* identifying clones that may be gene-rich and allows  
\* overlap relationships among clones to be deduced.  
\* However, it should not be assumed that this clone  
\* will be sequenced to completion. In the event that  
\* the record is updated, the accession number will  
\* be preserved.

\* 1 868: contig of 868 bp in length  
\* 869 968: gap of 100 bp  
\* 969 1903: contig of 935 bp in length  
\* 1904 2003: gap of 100 bp  
\* 2004 2884: contig of 881 bp in length  
\* 2885 2984: gap of 100 bp  
\* 2985 3916: contig of 932 bp in length  
\* 3917 4016: gap of 100 bp  
\* 4017 4937: contig of 921 bp in length  
\* 4938 5037: gap of 100 bp  
\* 5038 5940: contig of 903 bp in length  
\* 5941 6040: gap of 100 bp  
\* 6041 6959: contig of 919 bp in length  
\* 6960 7059: gap of 100 bp  
\* 7060 7974: contig of 915 bp in length  
\* 7975 8074: gap of 100 bp  
\* 8075 9019: contig of 945 bp in length  
\* 9020 9119: gap of 100 bp  
\* 9120 10046: contig of 927 bp in length  
\* 10047 10146: gap of 100 bp  
\* 10147 11053: contig of 907 bp in length  
\* 11054 11153: gap of 100 bp  
\* 11154 12059: contig of 906 bp in length  
\* 12060 12159: gap of 100 bp  
\* 12160 13077: contig of 918 bp in length



JOURNAL  
REFERENCE  
AUTHORS  
  
TITLE  
JOURNAL

Published Only in DataBase (2000)  
2 (bases 1 to 211452)  
Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P.,  
Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.  
Direct Submission  
Submitted (08-MAY-2000) Masahira Hattori, The Institute of Physical  
and Chemical Research (RIKEN), Genomic Sciences Center (GSC);  
Kitasato Univ., 1-15-1 Kitasato, Sagamihara, Kanagawa 228-8555,  
Japan (E-mail:hattori@gsc.riken.go.jp,  
URL:http://hgp.gsc.riken.go.jp/, Tel:81-42-778-9923,  
Fax:81-42-778-9924)  
On May 30, 2000 this sequence version replaced gi:7768935.

COMMENT

----- Genome Center  
Center: RIKEN Genomic Sciences Center(GSC)  
Center code: RIKEN  
Web site: http://hgp.gsc.riken.go.jp/  
Contact: hattori@gsc.riken.go.jp  
----- Project Information  
Center project name: HumDraft11  
Center clone name: RP11-880P3  
----- Summary Statistics  
Sequencing vector: PCR products; 100% of reads  
Chemistry: Dye-terminator ET-amersham; 100% of reads  
Assembly program: Phrap; version 0.990329  
Consensus quality: 189257 bases at least Q40  
Consensus quality: 200319 bases at least Q30  
Consensus quality: 205564 bases at least Q20  
Insert size: 208152; sum-of-contigs  
Quality coverage: 4.07x in Q20 bases; sum-of-contigs  
-----

NOTE: This is a 'working draft' sequence. It currently consists of  
34 contigs. The true order of the pieces is not known and their  
order in this sequence record is arbitrary. Gaps between the  
contigs are represented as runs N, but the exact sizes of the gaps  
are unknown. This record will be updated with the finished sequence  
as soon as it is available and the accession number will be  
preserved

1 28021 contig of 28021 bp in length  
28122 42064 contig of 13943 bp in length  
42165 54544 contig of 12380 bp in length  
54645 66934 contig of 12290 bp in length  
67035 78065 contig of 11031 bp in length  
78166 85965 contig of 7800 bp in length  
86066 94021 contig of 7956 bp in length  
94122 103137 contig of 9016 bp in length  
103238 110428 contig of 7191 bp in length  
110529 117261 contig of 6733 bp in length  
117362 124135 contig of 6774 bp in length  
124236 130599 contig of 6364 bp in length  
130700 136620 contig of 5921 bp in length  
136721 143251 contig of 6531 bp in length  
143352 149360 contig of 6009 bp in length  
149461 154813 contig of 5353 bp in length  
154914 160814 contig of 5901 bp in length  
160915 165830 contig of 4916 bp in length  
165931 171277 contig of 5347 bp in length  
171278 171377 contig of 3641 bp in length  
171978 175018 contig of 3641 bp in length  
175019 175118 contig of 100 bp  
175119 179182 contig of 4064 bp in length  
179183 179282 contig of 100 bp  
179283 183958 contig of 4676 bp in length  
183959 184058 contig of 100 bp  
184059 188202 contig of 4144 bp in length  
188203 188302 contig of 100 bp  
188303 191129 contig of 2827 bp in length  
191130 191229 contig of 100 bp  
191230 194326 contig of 3097 bp in length  
194327 194426 contig of 100 bp  
194427 197543 contig of 3117 bp in length  
179283 183958 contig of 4676 bp in length  
184059 188202 contig of 4144 bp in length  
188303 191129 contig of 2827 bp in length  
191230 194326 contig of 3097 bp in length  
194427 197543 contig of 3117 bp in length  
197644 200559 contig of 2916 bp in length  
200660 203056 contig of 2397 bp in length  
203157 205136 contig of 1980 bp in length  
205237 206801 contig of 1565 bp in length  
206902 207589 contig of 688 bp in length  
207690 209148 contig of 1459 bp in length  
209249 210259 contig of 1011 bp in length  
210360 211452 contig of 1093 bp in length

Sequence updated (26-May-2000).

\* NOTE: This is a 'working draft' sequence. It currently

\* consists of 34 contigs. The true order of the pieces  
\* is not known and their order in this sequence record is  
\* arbitrary. Gaps between the contigs are represented as  
\* runs of N, but the exact sizes of the gaps are unknown.  
\* This record will be updated with the finished sequence  
\* as soon as it is available and the accession number will  
\* be preserved.

1 28021: contig of 28021 bp in length  
28022 28121: gap of 100 bp  
28122 42064: contig of 13943 bp in length  
42065 42164: gap of 100 bp  
42165 54544: contig of 12380 bp in length  
54545 54644: gap of 100 bp  
54645 66934: contig of 12290 bp in length  
66935 67034: gap of 100 bp  
67035 78065: contig of 11031 bp in length  
78066 78165: gap of 100 bp  
78166 85965: contig of 7800 bp in length  
85966 86065: gap of 100 bp  
86066 94021: contig of 7956 bp in length  
94022 94121: gap of 100 bp  
94122 103137: contig of 9016 bp in length  
103138 103237: gap of 100 bp  
103238 110428: contig of 7191 bp in length  
110429 110528: gap of 100 bp  
110529 117261: contig of 6733 bp in length  
117262 117361: gap of 100 bp  
117362 124135: contig of 6774 bp in length  
124136 124235: gap of 100 bp  
124236 130599: contig of 6364 bp in length  
130600 130699: gap of 100 bp  
130700 136620: contig of 5921 bp in length  
136621 136720: gap of 100 bp  
136721 143251: contig of 6531 bp in length  
143252 143351: gap of 100 bp  
143352 149360: contig of 6009 bp in length  
149361 149460: gap of 100 bp  
149461 154813: contig of 5353 bp in length  
154814 154913: gap of 100 bp  
154914 160814: contig of 5901 bp in length  
160815 160914: gap of 100 bp  
160915 165830: contig of 4916 bp in length  
165831 165930: gap of 100 bp  
165931 171277: contig of 5347 bp in length  
171278 171377: gap of 100 bp  
171978 175018: contig of 3641 bp in length  
175019 175118: gap of 100 bp  
175119 179182: contig of 4064 bp in length  
179183 179282: gap of 100 bp  
179283 183958: contig of 4676 bp in length  
183959 184058: gap of 100 bp  
184059 188202: contig of 4144 bp in length  
188203 188302: gap of 100 bp  
188303 191129: contig of 2827 bp in length  
191130 191229: gap of 100 bp  
191230 194326: contig of 3097 bp in length  
194327 194426: gap of 100 bp  
194427 197543: contig of 3117 bp in length  
197544 197643: gap of 100 bp  
197644 200559: contig of 2916 bp in length  
200560 200659: gap of 100 bp  
200660 203056: contig of 2397 bp in length  
203057 203156: gap of 100 bp  
203157 205136: contig of 1980 bp in length  
205137 205236: gap of 100 bp  
205237 206801: contig of 1565 bp in length  
206802 206901: gap of 100 bp  
206902 207589: contig of 688 bp in length  
207590 209148: gap of 100 bp  
209149 209248: gap of 100 bp  
209249 210259: contig of 1011 bp in length  
210260 210359: gap of 100 bp











McCarthy,M., McEwan,P., McGurk,A., McKernan,K., MCPheeters,R.,  
Meldrim,J., Meneus,L., Mihova,T., Miranda,C., Mlenga,V., Morrow,J.,  
Murphy,T., Naylor,J., Norman,C.H., O'Connor,T., O'Donnell,P.,  
O'Neil,D., Ollivar,T.M., Oliver,J., Peterson,K., Pierre,N.,  
Pisani,C., Pollara,V., Raymond,C., Riley,R., Rogov,P., Rothman,D.,  
Roy,A., Santos,R., Schauer,S., Severy,P., Spencer,B.,  
Stange-Thomann,N., Stojanovic,N., Subramanian,A., Talamas,J.,  
Tessfaye,S., Theodore,J., Tirrell,A., Travers,M., Trigilio,J.,  
Vassiliev,H., Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J.,  
Young,G., Zainoun,J., Zimmer,A. and Zody,M.  
Direct Submission

TITLE  
JOURNAL

Submitted (01-APR-2000) Whitehead Institute/MIT Center for Genome  
Research, 320 Charles Street, Cambridge, MA 02141, USA  
All repeats were identified using RepeatMasker:  
Smit, A.F.A. & Green, P. (1996-1997)  
<http://ftp.genome.washington.edu/RM/RepeatMasker.html>

COMMENT

----- Genome Center  
Center: Whitehead Institute/ MIT Center for Genome Research  
Center code: WIBR  
Web site: <http://www-seq.wi.mit.edu>  
Contact: [sequence\\_submissions@genome.wi.mit.edu](mailto:sequence_submissions@genome.wi.mit.edu)  
----- Project Information  
Center project name: L8146  
Center clone name: 440\_H\_3  
-----

\* NOTE: This record contains 86 individual  
\* sequencing reads that have not been assembled into  
\* contigs. Runs of N are used to separate the reads  
\* and the order in which they appear is completely  
\* arbitrary. Low-pass sequence sampling is useful for  
\* identifying clones that may be gene-rich and allows  
\* overlap relationships among clones to be deduced.  
\* However, it should not be assumed that this clone  
\* will be sequenced to completion. In the event that  
\* the record is updated, the accession number will  
\* be preserved.

1 694: contig of 694 bp in length  
695 794: gap of 100 bp  
795 1531: contig of 737 bp in length  
1532 1631: gap of 100 bp  
1632 2364: contig of 733 bp in length  
2365 2464: gap of 100 bp  
2465 3205: contig of 741 bp in length  
3206 3305: gap of 100 bp  
3306 4012: contig of 707 bp in length  
4013 4112: gap of 100 bp  
4113 4818: contig of 706 bp in length  
4819 4918: gap of 100 bp  
4919 5609: contig of 691 bp in length  
5610 5709: gap of 100 bp  
5710 6413: contig of 704 bp in length  
6414 6513: gap of 100 bp  
6514 7217: contig of 704 bp in length  
7218 7317: gap of 100 bp  
7318 8038: contig of 721 bp in length  
8039 8138: gap of 100 bp  
8139 8844: contig of 706 bp in length  
8845 8944: gap of 100 bp  
8945 9653: contig of 709 bp in length  
9654 9753: gap of 100 bp  
9754 10471: contig of 718 bp in length  
10472 10571: gap of 100 bp  
10572 11253: contig of 682 bp in length  
11254 11353: gap of 100 bp  
11354 12069: contig of 716 bp in length  
12070 12169: gap of 100 bp  
12170 12877: contig of 708 bp in length  
12878 12977: gap of 100 bp  
12978 13684: contig of 707 bp in length  
13685 13784: gap of 100 bp  
13785 14479: contig of 695 bp in length  
14480 14579: gap of 100 bp  
14580 15302: contig of 723 bp in length

15303 15402: gap of 100 bp  
15403 16107: contig of 705 bp in length  
16108 16207: gap of 100 bp  
16208 16930: contig of 723 bp in length  
16931 17030: gap of 100 bp  
17031 17766: contig of 736 bp in length  
17767 17866: gap of 100 bp  
17867 18590: contig of 724 bp in length  
18591 18690: gap of 100 bp  
18691 19399: contig of 709 bp in length  
19400 19499: gap of 100 bp  
19500 20201: contig of 702 bp in length  
20202 20301: gap of 100 bp  
20302 21002: contig of 701 bp in length  
21003 21102: gap of 100 bp  
21103 21817: contig of 715 bp in length  
21818 21917: gap of 100 bp  
21918 22597: contig of 680 bp in length  
22598 22697: gap of 100 bp  
22698 23383: contig of 686 bp in length  
23384 23483: gap of 100 bp  
23484 24180: contig of 697 bp in length  
24181 24280: gap of 100 bp  
24281 24993: contig of 713 bp in length  
24994 25093: gap of 100 bp  
25094 25809: contig of 716 bp in length  
25810 25909: gap of 100 bp  
25910 26637: contig of 728 bp in length  
26638 26737: gap of 100 bp  
26738 27446: contig of 709 bp in length  
27447 27546: gap of 100 bp  
27547 28264: contig of 718 bp in length  
28265 28364: gap of 100 bp  
28365 29079: contig of 715 bp in length  
29080 29179: gap of 100 bp  
29180 29913: contig of 734 bp in length  
29914 30013: gap of 100 bp  
30014 30729: contig of 716 bp in length  
30730 30829: gap of 100 bp  
30830 31524: contig of 695 bp in length  
31525 31624: gap of 100 bp  
31625 32335: contig of 711 bp in length  
32336 32435: gap of 100 bp  
32436 33140: contig of 705 bp in length  
33141 33240: gap of 100 bp  
33241 33946: contig of 706 bp in length  
33947 34046: gap of 100 bp  
34047 34755: contig of 709 bp in length  
34756 34855: gap of 100 bp  
34856 35561: contig of 706 bp in length  
35562 35661: gap of 100 bp  
35662 36376: contig of 715 bp in length  
36377 36476: gap of 100 bp  
36477 37199: contig of 723 bp in length  
37200 37299: gap of 100 bp  
37300 38018: contig of 719 bp in length  
38019 38118: gap of 100 bp  
38119 38828: contig of 710 bp in length  
38829 38928: gap of 100 bp  
38929 39636: contig of 708 bp in length  
39637 39736: gap of 100 bp  
39737 40449: contig of 713 bp in length  
40450 40549: gap of 100 bp  
40550 41255: contig of 706 bp in length  
41256 41355: gap of 100 bp  
41356 42068: contig of 713 bp in length  
42069 42168: gap of 100 bp  
42169 42873: contig of 705 bp in length  
42874 42973: gap of 100 bp  
42974 43694: contig of 721 bp in length  
43695 43794: gap of 100 bp  
43795 44510: contig of 716 bp in length  
44511 44610: gap of 100 bp



\* 18021 18736: contig of 716 bp in length  
\* 18737 18836: gap of 100 bp  
\* 18837 19563: contig of 727 bp in length  
\* 19564 19663: gap of 100 bp  
\* 19664 20411: contig of 748 bp in length  
\* 20412 20511: gap of 100 bp  
\* 20512 21253: contig of 742 bp in length  
\* 21254 21353: gap of 100 bp  
\* 21354 22070: contig of 717 bp in length  
\* 22071 22170: gap of 100 bp  
\* 22171 22874: contig of 704 bp in length  
\* 22875 22974: gap of 100 bp  
\* 22975 23686: contig of 712 bp in length  
\* 23687 23786: gap of 100 bp  
\* 23787 24499: contig of 713 bp in length  
\* 24500 24599: gap of 100 bp  
\* 24600 25290: contig of 691 bp in length  
\* 25291 25390: gap of 100 bp  
\* 25391 26114: contig of 724 bp in length  
\* 26115 26214: gap of 100 bp  
\* 26215 26932: contig of 718 bp in length  
\* 26933 27032: gap of 100 bp  
\* 27033 27761: contig of 729 bp in length  
\* 27762 27861: gap of 100 bp  
\* 27862 28568: contig of 707 bp in length  
\* 28569 28668: gap of 100 bp  
\* 28669 29396: contig of 728 bp in length  
\* 29397 29496: gap of 100 bp  
\* 29497 30228: contig of 732 bp in length  
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\* 30329 31045: contig of 717 bp in length  
\* 31046 31145: gap of 100 bp  
\* 31146 31845: contig of 700 bp in length  
\* 31846 31945: gap of 100 bp  
\* 31946 32628: contig of 683 bp in length  
\* 32629 32728: gap of 100 bp  
\* 32729 33454: contig of 726 bp in length  
\* 33455 33554: gap of 100 bp  
\* 33555 34265: contig of 711 bp in length  
\* 34266 34366: contig of 100 bp  
\* 34366 35063: contig of 698 bp in length  
\* 35064 35163: gap of 100 bp  
\* 35164 35863: contig of 700 bp in length  
\* 35864 35963: gap of 100 bp  
\* 35964 36682: contig of 719 bp in length  
\* 36683 36782: gap of 100 bp  
\* 36783 37489: contig of 707 bp in length  
\* 37490 37589: gap of 100 bp  
\* 37590 38325: contig of 736 bp in length  
\* 38326 38425: gap of 100 bp  
\* 38426 39178: contig of 753 bp in length  
\* 39179 39278: gap of 100 bp  
\* 39279 39999: contig of 721 bp in length  
\* 40000 40099: gap of 100 bp  
\* 40100 40804: contig of 705 bp in length  
\* 40805 40904: gap of 100 bp  
\* 40905 41594: contig of 690 bp in length  
\* 41595 41694: gap of 100 bp  
\* 41695 42405: contig of 711 bp in length  
\* 42406 42505: gap of 100 bp  
\* 42506 43224: contig of 719 bp in length  
\* 43225 43324: gap of 100 bp  
\* 43325 44033: contig of 709 bp in length  
\* 44034 44133: gap of 100 bp  
\* 44134 44834: contig of 701 bp in length  
\* 44835 44934: gap of 100 bp  
\* 44935 45670: contig of 736 bp in length  
\* 45671 45770: gap of 100 bp  
\* 45771 46500: contig of 730 bp in length  
\* 46501 46600: gap of 100 bp  
\* 46601 47331: contig of 731 bp in length  
\* 47332 47431: gap of 100 bp  
\* 47432 48172: contig of 741 bp in length

\* 48173 48272: gap of 100 bp  
\* 48273 49033: contig of 761 bp in length  
\* 49034 49133: gap of 100 bp  
\* 49134 49812: contig of 679 bp in length  
\* 49813 49912: gap of 100 bp  
\* 49913 50599: contig of 687 bp in length  
\* 50600 50699: gap of 100 bp  
\* 50700 51420: contig of 721 bp in length  
\* 51421 51520: gap of 100 bp  
\* 51521 52252: contig of 732 bp in length  
\* 52253 52352: gap of 100 bp  
\* 52353 53054: contig of 702 bp in length  
\* 53055 53154: gap of 100 bp  
\* 53155 53862: contig of 708 bp in length  
\* 53863 53962: gap of 100 bp  
\* 53963 54697: contig of 735 bp in length  
\* 54698 54797: gap of 100 bp  
\* 54798 55557: contig of 760 bp in length  
\* 55558 55657: gap of 100 bp  
\* 55658 56366: contig of 709 bp in length  
\* 56367 56466: gap of 100 bp  
\* 56467 57164: contig of 698 bp in length

Query Match 13.9%; Score 35; DB 2; Length 70125;  
Best Local Similarity 100.0%; Pred. No. 3.2e-09;  
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 90 ACAAAAAATCNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 124  
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Db 66041 ACAAAAAATCNNNNNNNNNNNNNNNNNNNNNNNNNNNN 66075

RESULT 7  
AC144333/c

LOCUS AC144333 136479 bp DNA linear HTG 09-APR-2003  
DEFINITION Macaca mulatta clone CH250-271N4, \*\*\* SEQUENCING IN PROGRESS \*\*\*.  
ACCESSION AC144333  
VERSION AC144333.1 GI:29650221  
KEYWORDS HTG; HTGS PHASE2; HTGS\_PGI.  
SOURCE Macaca mulatta (rhesus monkey)  
ORGANISM Macaca mulatta  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;  
Cercopithecinae; Macaca.

REFERENCE 1 (bases 1 to 136479)  
AUTHORS Csuros,M. and Milosavljevic,A.  
TITLE Pooled genomic indexing (PGI): mathematical analysis and experiment design

JOURNAL (in) Guigo,R. and Gusfield,D. (Eds.);  
ALGORITHMS IN BIOINFORMATICS, SECOND INTERNATIONAL WORKSHOP, WABI  
2002, ROME, ITALY, SEPTEMBER 17-21, 2002, PROCEEDINGS: 10-28;  
Springer (2002)

REFERENCE 2 (bases 1 to 136479)  
AUTHORS Milosavljevic,A., Sodergren,E., Csuros,M., Li,B., Jackson,A.R.,  
Adams,C., Adio-Oduola,B., Ali-osman,F.R., Allen,C., Alsbrooks,S.L.,  
Amaratunge,H.C., Are,J.R., Ayele,M., Banks,T., Barbaria,J.,  
Benton,J., Bimage,K., Blankenburg,K., Bonnir,D., Bouck,J.,  
Bowie,S., Brieva,M., Brown,E., Brown,M., Bryant,N.P., Buhay,C.,  
Burch,P., Burkett,C., Burrell,K.L., Byrd,N.C., Carron,T.F.,  
Carter,M., Cavazos,S.R., Chacko,J., Chavez,D., Chen,G., Chen,R.,  
Chen,Z., Chiu,D., Chowdhry,I., Christopoulos,C., Cleveland,C.D.,  
Cox,C., Coyle,M.D., Dathorne,S.R., David,R., Davila,M.L., Davis,C.,  
Davy-Carroll,L., Dederich,D.A., Delaney,K.R., Delgado,O.,  
Denn,A.L., Ding,Y., Dinh,H.H., Douthwaite,K.J., Draper,H.,  
Dugan-Rocha,S., Durbin,K.J., Egan,A., Earnhart,C., Edwards,C.C.,  
Elhaj,C., Emerling,S., Escotto,M., Falls,T., Ferraguto,D.,  
Flagg,N., Ford,J., Foster,P., Frantz,P., Gabisi,A., Gao,J.,  
Garcia,A., Garner,T., Garza,N., Gill,P., Gorrell,J.H., Guevara,W.,  
Gunaratne,P., Hale,S., Hamilton,K., Han,J., Harris,C., Harris,K.,  
Hart,M., Havlak,P., Hawes,A., Hernandez,J., Hernandez,O.,  
Hodgson,A., Hognes,M., Holloway,C., Hollins,B., Homs,F.,  
Howard,S., Huber,J., Hulyk,S., Hume,J., Ioshikhes,I., Jackson,L.E.,  
Jacobson,B., Jia,Y., Johnson,R., Jolivet,S., Joudah,S.,







```
RESULT 9
AC093306      158231 bp      DNA      linear      HTG 16-AUG-2001
LOCUS      Homo sapiens chromosome 5 clone RP11-71K19, WORKING DRAFT SEQUENCE,
DEFINITION      4 unordered pieces.
ACCESSION      AC093306
VERSION      AC093306.1 GI:15193440
KEYWORDS      HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ACTIVEFIN.
SOURCE      Homo sapiens (human)
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 158231)
DOE Joint Genome Institute.
Sequencing of Human Chromosome 5
Unpublished
2 (bases 1 to 158231)
DOE Joint Genome Institute.
Direct Submission
Submitted (16-AUG-2001) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
-----Genome Center
Center: Joint Genome Institute
Center Code: JGI
Web site: http://www.jgi.doe.gov
-----
Project Information
Center Project Name: 43388
Center clone name: RPCI-11_71K19
-----
Summary Statistics
Consensus quality: 155197 bases at least Q40
Consensus quality: 156495 bases at least Q30
Consensus quality: 157279 bases at least Q20
Estimated insert size: 167260; agarose-fp estimation
Quality coverage: 11.02 in Q20 bases; agarose-fp estimation
Quality coverage: 11.67 in Q20 bases; sum-of-contigs estimation.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 4 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
* 1 1000: contig of 1000 bp in length
* 1001 1100: gap of unknown length
* 1101 2270: contig of 1170 bp in length
* 2271 2370: gap of unknown length
* 2371 14042: contig of 11672 bp in length
* 14043 14142: gap of unknown length
* 14143 158231: contig of 144089 bp in length.
FEATURES
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Location/Qualifiers
1..158231
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="5"
/clone="RP11-71K19"
/clone_lib="RPCI human BAC library 11"
BASE COUNT 47582 a 2902i c 28686 g 52623 t 319 others
ORIGIN
Query Match 13.9%; Score 35; DB 2; Length 158231;
Best Local Similarity 100.0%; Pred. No. 2.9e-09;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
90 ACAAAAATCNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 124
|||||
991 ACAAAAATCNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 1025
|||||
```

```
RESULT 10
AC124963      160191 bp      DNA      linear      HTG 14-MAY-2003
LOCUS      Medicago truncatula clone mth2-24f5, WORKING DRAFT SEQUENCE, 6
DEFINITION      ordered pieces.
ACCESSION      AC124963
VERSION      AC124963.12 GI:30698573
KEYWORDS      HTG; HTGS_PHASE2; HTGS_DRAFT.
SOURCE      Medicago truncatula (barrel medic)
ORGANISM      Medicago truncatula
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
Medicago.
1 (bases 1 to 160191)
Shauli,S., Lin,S., Dixon,R., May,G., Sumner,L., Gonzales,B.,
Cook,D., Kim,D. and Roe,B.A.
Medicago truncatula BAC Clone mth2-24f5
Unpublished
2 (bases 1 to 160191)
Shauli,S., Lin,S., Dixon,R., May,G., Sumner,L., Gonzales,B.,
Cook,D., Kim,D. and Roe,B.A.
Direct Submission
Submitted (20-JUN-2002) Department Of Chemistry And Biochemistry,
The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman,
OK 73019, USA
3 (bases 1 to 160191)
Shauli,S., Lin,S., Dixon,R., May,G., Sumner,L., Gonzales,B.,
Cook,D., Kim,D. and Roe,B.A.
Direct Submission
Submitted (14-MAY-2003) Department Of Chemistry And Biochemistry,
The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman,
OK 73019, USA
On May 14, 2003 this sequence version replaced gi:30387683.
----- Genome Center
Center: Department Of Chemistry And Biochemistry
The University Of Oklahoma
Center code:UOKNOR
-----
* NOTE: This is a 'working draft' sequence. It currently
* consists of 6 contigs. Gaps between the contigs
* are represented as runs of N. The order of the pieces
* is believed to be correct as given, however the sizes
* of the gaps between them are based on estimates that have
* provided by the submittor.
* This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved.
* 1 13168: contig of 13168 bp in length
* 13169 13268: gap of unknown length
* 13269 29072: contig of 15804 bp in length
* 29073 29172: gap of unknown length
* 29173 50317: contig of 21145 bp in length
* 50318 50417: gap of unknown length
* 50418 74728: contig of 24311 bp in length
* 74729 74828: gap of unknown length
* 74829 115700: contig of 40872 bp in length
* 115701 115800: gap of unknown length
* 115801 160191: contig of 44391 bp in length.
FEATURES
source
Location/Qualifiers
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/organism="Medicago truncatula"
/mol_type="genomic DNA"
/db_xref="taxon:3880"
/clone="mth2-24f5"
/clone_lib="Medicago truncatula BAC library H2"
BASE COUNT 53000 a 26397 c 26913 g 53374 t 507 others
ORIGIN
Query Match 13.9%; Score 35; DB 2; Length 160191;
Best Local Similarity 100.0%; Pred. No. 2.9e-09;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

[illegible]







COURCE	Rattus norvegicus (Norway rat)	----- Project Information
ORGANISM	Rattus norvegicus	Center project name: KDPK
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	Center clone name: CH230-6318
	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;	----- Summary Statistics
	Rattus.	Sequencing vector: Plasmid;
EPERENCE	1 (bases 1 to 230154)	Chemistry: Dye-terminator Big Dye: 100% of reads
AUTHORS	Muzny,D.Marie., Metzker,M.Lee., Abramzon,S., Adams,C., Alder,J., Allen,C., Allen,H., Alsbrooks,S., Amin,A., Anguiano,D., Anyalebechi,V., Aoyagi,A., Ayodeji,M., Baca,E., Baden,H., Baldwin,D., Bandaranaike,D., Barber,M., Barnstead,M., Benahmed,F., Biswal,K., Blair,J., Blankenburg,K., Blyth,P., Brown,M., Bryant,N., Buhay,C., Burch,P., Burrell,K., Calderon,E., Cardenas,V., Carter,K., Cavazos,I., Ceasar,H., Center,A., Chacko,J., Chavez,D., Chen,G., Chen,R., Chen,Y., Chen,Z., Chu,J., Cleveland,C., Cockrell,R., Cox,C., Coyle,M., Cree,A., D'Souza,L., Davila,M.L., Davis,C., Davy-Carroll,L., De Anda,C., Dederich,D., Delgado,O., Denson,S., Deramo,C., Ding,Y., Dinh,H., Divya,K., Draper,H., Dugan-Rocha,S., Dunn,A., Durbin,K., Duval,B., Eaves,K., Egan,A., Escotto,M., Eugene,C., Evans,C.A., Falls,T., Fan,G., Fernandez,S., Finley,M., Flagg,N., Forbes,L., Foster,M., Foster,P., Fraser,C.M., Gabisi,A., Ganta,R., Garcia,A., Garner,T., Garza,M., Gebregeorgis,E., Geer,K., Gill,R., Grady,M., Guerra,W., Guevara,W., Gunaratne,P., Haaland,W., Hamil,C., Hamilton,C., Hamilton,K., Harvey,Y., Havlak,P., Hawes,A., Henderson,N., Hernandez,J., Hernandez,R., Hines,S., Hladun,S.L., Hodgson,A., Hognes,M., Hollins,B., Howells,S., Hulyk,S., Hume,J., Idlebird,D., Jackson,A., Jackson,L., Jacob,L., Jiang,H., Johnson,B., Johnson,R., Jolivet,A., Karpathy,S., Kelly,S., Kelly,S., Khan,Z., King,L., Kovar,C., Kowis,C., Kraft,C.L., Lebow,H., Levan,J., Lewis,L., Li,Z., Liu,J., Liu,J., Liu,W., Liu,Y., London,P., Longacre,S., Lopez,J., Lorensuhewa,L., Loulseged,H., Lozado,R.J., Lu,X., Ma,J., Maheshwari,M., Mahindartne,M., Mahmoud,M., Malloy,K., Mangum,A., Mangum,B., Mapua,P., Martin,K., Martin,R., Martinez,E., Mawhiney,S., Mcleod,M., McNeill,T., Meenen,E., Milosavljevic,A., Miner,G., Minja,E., Montemayor,J., Moore,S., Morgan,M., Morris,K., Morris,S., Munidasa,M., Murphy,M., Nair,L., Nankervis,C., Neal,D., Newton,N., Nguyen,N., Norris,S., Nwaokeleneh,O., Okwuonu,G., Olarnpunsagoon,A., Pal,S., Parks,K., Pasternak,S., Paul,H., Perez,A., Perez,L., Pfannkoch,C., Plopper,F., Poindexter,A., Popovic,D., Primus,E., Pu,L.-L., Puazo,M., Quiroz,J., Rachlin,E., Reeves,K., Regier,M.A., Reigh,R., Reilly,B., Reilly,M., Ren,Y., Reuter,M., Richards,S., Riggs,F., Rives,C., Rodkey,T., Rojas,A., Rose,M., Rose,R., Ruiz,S.J., Sanders,W., Savery,G., Scherer,S., Scott,G., Shatsman,S., Shen,H., Shetty,J., Shvartsbeyn,A., Sisson,I., Sitter,C.D., Smajs,D., Sneed,A., Sodergren,E., Song,X.-Z., Sorelle,R., Sosa,J., Steimle,M., Strong,R., Sutton,A., Svatek,A., Tabor,P., Taylor,C., Taylor,T., Thomas,N., Thomas,S., Tingey,A., Trejos,Z., Usmani,K., Valas,R., Vera,V., Villasana,D., Waldron,L., Walker,B., Wang,J., Wang,Q., Wang,S., Warren,J., Warren,R., Wei,X., White,F., Williams,G., Willson,R., Wleczyk,R., Wooden,H., Worley,K., Wright,D., Wright,R., Wu,J., Yakub,S., Yen,J., Yoon,L., Yoon,V., Yu,F., Zhang,J., Zhou,J., Zhou,X., Zhao,S., Dunn,D., von Niederhausern,A., Weiss,R., Smith,D.R., Holt,R.A., Smith,H.O., Weinstock,G. and Gibbs,R.A.	-----
TITLE	Direct Submission	
JOURNAL	Unpublished	
REFERENCE	2 (bases 1 to 230154)	
AUTHORS	Worley,K.C.	
TITLE	Direct Submission	
JOURNAL	Submitted (28-FEB-2003) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA	
REFERENCE	3 (bases 1 to 230154)	
AUTHORS	Worley,K.C.	
TITLE	Direct Submission	
JOURNAL	Submitted (27-MAR-2003) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA	
COMMENT	----- Genome Center	
	Center: Baylor College of Medicine	
	Center code: BCM	
	Web site: <a href="http://www.hgsc.bcm.tmc.edu/">http://www.hgsc.bcm.tmc.edu/</a>	
	Contact: <a href="mailto:hgsc-help@bcm.tmc.edu">hgsc-help@bcm.tmc.edu</a>	

1	1121:	contig of 1121 bp in length
*	1122	1221: gap of unknown length
*	1222	2311: contig of 1090 bp in length
*	2312	2411: gap of unknown length
*	2412	3545: contig of 1134 bp in length
*	3546	3645: gap of unknown length
*	3646	4881: contig of 1236 bp in length
*	4882	4981: gap of unknown length
*	4982	6010: contig of 1029 bp in length
*	6011	6110: gap of unknown length
*	6111	7203: contig of 1093 bp in length
*	7204	7303: gap of unknown length
*	7304	8496: contig of 1193 bp in length
*	8497	8596: gap of unknown length
*	8597	10255: contig of 1659 bp in length
*	10256	10355: gap of unknown length
*	10356	11809: contig of 1454 bp in length
*	11810	11909: gap of unknown length
*	11910	13265: contig of 1356 bp in length
*	13266	13365: gap of unknown length
*	13366	15347: contig of 1982 bp in length
*	15348	15447: gap of unknown length
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*	16841	16940: gap of unknown length
*	16941	18100: contig of 1160 bp in length
*	18101	18200: gap of unknown length
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*	19781	19880: gap of unknown length
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*	36790	36889: gap of unknown length
*	36890	38922: contig of 2033 bp in length
*	38923	39022: gap of unknown length
*	39023	41368: contig of 2346 bp in length
*	41369	41468: gap of unknown length

\* 41469 43309: contig of 1841 bp in length  
\* 43310 43409: gap of unknown length  
\* 43410 44931: contig of 1522 bp in length  
\* 44932 45031: gap of unknown length  
\* 45032 46557: contig of 1526 bp in length  
\* 46558 46657: gap of unknown length  
\* 46658 48429: contig of 1772 bp in length  
\* 48430 48529: gap of unknown length  
\* 48530 50022: contig of 1493 bp in length  
\* 50023 50122: gap of unknown: length  
\* 50123 52297: contig of 2175 bp in length  
\* 52298 52397: gap of unknown length  
\* 52398 54714: contig of 2317 bp in length  
\* 54715 54814: gap of unknown length  
\* 54815 57089: contig of 2275 bp in length  
\* 57090 57189: gap of unknown length  
\* 57190 59531: contig of 2342 bp in length  
\* 59532 59631: gap of unknown length  
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\* 61795 61894: gap of unknown length  
\* 61895 64480: contig of 2586 bp in length  
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\* 94170 94269: gap of unknown length  
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\* 101122 101221: gap of unknown length  
\* 101222 104888: contig of 3667 bp in length  
\* 104889 104988: gap of unknown length

Query Match 13.9%; Score 35; DB 2; Length 230154;  
Best Local Similarity 100.0%; Pred. No. 2.8e-09;  
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 90 ACAAAAAATCNNNNNNNNNNNNNNNNNNNNNNNNNN 124  
DD 15338 ACAAAAAATCNNNNNNNNNNNNNNNNNNNNNNNN 15372

RESULT 14  
AC094936/6  
LOCUS AC094936 236385 bp DNA linear HTG 09-MAY-2003  
DEFINITION Rattus norvegicus clone CH230-6E5, WORKING DRAFT SEQUENCE, 2  
unordered pieces.  
AC094936  
AC094936.6 GI:30466971  
HTG; HTGS\_PHASE1; HTGS\_DRAFT; HTGS\_FULLTOP.  
KEYWORDS Rattus norvegicus (Norway rat)  
SOURCE Rattus norvegicus  
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;  
Rattus.  
REFERENCE 1 (bases 1 to 236385)  
AUTHORS Muzny,D.Marie., Metzker,M.Lee., Abramzon,S., Adams,C., Alder,J.,

Allen,C., Allen,H., Alsbrooks,S., Amin,A., Anguiano,D.,  
Anyalebechi,V., Aoyagi,A., Ayodeji,M., Baca,E., Baden,H.,  
Baldwin,D., Bandaranaike,D., Barber,M., Barnstead,M., Benahmed,F.,  
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Davila,M.L., Davis,C., Davy-Carroll,L., De Anda,C., Dederich,D.,  
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Yu,F., Zhang,J., Zhou,J., Zhou,X., Zhao,S., Dunn,D., von  
Niederhausern,A., Weiss,R., Smith,D.R., Holt,R.A., Smith,H.O.,  
Weinstock,G. and Gibbs,R.A.  
Direct Submission  
Unpublished  
2 (bases 1 to 236385)  
Worley,K.C.  
Direct Submission  
Submitted (15-SEP-2001) Human Genome Sequencing Center, Department  
of Molecular and Human Genetics, Baylor College of Medicine, One  
Baylor Plaza, Houston, TX 77030, USA  
3 (bases 1 to 236385)  
Rat Genome Sequencing Consortium.  
Direct Submission  
Submitted (09-MAY-2003) Human Genome Sequencing Center, Department  
of Molecular and Human Genetics, Baylor College of Medicine, One  
Baylor Plaza, Houston, TX 77030, USA  
On May 9, 2003 this sequence version replaced gi:23101377.  
The sequence in this assembly is a combination of BAC based reads  
and whole genome shotgun sequencing reads assembled using Atlas  
(http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described  
in the feature table below represents a scaffold in the Atlas  
assembly (a 'contig-scaffold'). Within each contig-scaffold,  
individual sequence contigs are ordered and oriented, and separated  
by sized gaps filled with Ns to the estimated size. The sequence  
may extend beyond the ends of the clone and there may be sequence  
contigs within a contig-scaffold that consist entirely of whole  
genome shotgun sequence reads. Both end sequences and whole genome





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Consensus quality: 212971 bases at least Q20
Estimated insert size: 231715; sum-of-contigs estimation
Quality coverage: 5x in Q20 bases; sum-of-contigs estimation
-----
* NOTE: Estimated insert size may differ from sequence length
* (see http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html).
* NOTE: This is a 'working draft' sequence. It currently
* consists of 2 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
*
* 1 240340: contig of 240340 bp in length
* 240341 240440: gap of unknown length
* 240441 241607: contig of 1167 bp in length.
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                     clone_end:Sp6"
                     8585..9499
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                     clone_end:Sp6
                     site:EcoRI
     misc_feature      end_sequence:BH258466"
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                     /note="clone_boundary"
                     clone_end:T7
                     site:EcoRI
                     end_sequence:BH258465"
BASE COUNT    51902 a 52205 c 54669 g 55437 t 27394 others
ORIGIN

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Best Local Similarity 100.0%; Pred. No. 2.8e-09;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db      8190 ACAAAAAATC
      |||
Search completed: November 6, 2003, 04:42:46
Job time : 1505 secs
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GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

M nucleic - nucleic search, using sw model

un on: November 6, 2003, 03:23:24 ; Search time 180 Seconds  
(without alignments)  
3764.216 Million cell updates/sec

itle: US-09-960-481-5278  
erfect score: 251  
equence: 1 ggtgcagttgtgtgacaca.....gtaagaaganatcaaccgag 251

coring table: OLIGO\_NUC  
Gapop 60.0 , Gapext 60.0

earched: 2552756 seqs, 1349719017 residues

ord size : 0  
otal number of hits satisfying chosen parameters: 5105512

inimum DB seq length: 0  
aximum DB seq length: 2000000000

ost-processing: Listing first 1000 summaries

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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

result No.	Score	Query Match	Length	DB	ID	Description
1	32	12.7	67087	21	AAF22280	BAC containing rep
C 2	31	12.4	409	25	ACA57265	Human adipocyte Se
C 3	31	12.4	765	25	ABZ20367	Oncofetal CDNA se
C 4	31	12.4	1075	20	AAV99321	GDNFR-alpha CDNA c
5	31	12.4	1200	24	ABK10773	Human SCYA26 modif
6	31	12.4	1560	24	AAD43682	Human interleukin
C 7	31	12.4	2157	20	AAV99318	GDNFR-alpha CDNA c
C 8	31	12.4	2568	18	AAT88419	Human glial cell l

82 29 11.6 2757 23 ABV24523 Human prostate exp  
83 29 11.6 3169 24 AAS94918 Human DNA sequence  
c 84 29 11.6 4336 18 AAV74857 Staphylococcus aur  
c 85 29 11.6 4438 9 AAN82262 Alpha-2 plasmin in  
86 29 11.6 4708 6 AAN50415 Human acetyl choli  
87 29 11.6 4846 18 AAV74587 Staphylococcus aur  
88 29 11.6 4992 24 AAS94783 Human DNA sequence  
89 29 11.6 5394 25 ACA03953 cDNA downregulated  
90 29 11.6 5727 18 AAV74501 Staphylococcus aur  
c 91 29 11.6 6346 18 AAV74548 Staphylococcus aur  
c 92 29 11.6 6777 25 ABX63289 Human CDNA #289 di  
c 93 29 11.6 13999 14 AAQ43845 Plasmid pAH4611.  
94 29 11.6 33780 22 AAH24652 Nucleotide sequenc  
95 29 11.6 45862 25 ABX93110 Genomic DNA encodi  
96 29 11.6 57699 25 ABV75538 Human transporter  
c 97 29 11.6 121001 21 AAF22284 BAC containing rep  
98 29 11.6 487980 25 AAD53223 Human chromosome 3  
99 28 11.2 49 24 ABK70501 In-situ analysis s  
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c 102 28 11.2 70 21 AAAG0395 HLA class II DRA p  
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120 28 11.2 77 20 AAX01791 Oligonucleotide 30  
121 28 11.2 77 20 AAV79638 Starting RNA seque  
122 28 11.2 77 21 AAA92738 HSV-1 DNA polymera  
123 28 11.2 77 21 AAA13672 GMPS-RNA molecule  
124 28 11.2 77 21 AAZ52749 Randomised nucleot  
125 28 11.2 77 22 AAF73456 Hepatocyte growth  
126 28 11.2 77 22 AAF70539 SELEX experiment o  
127 28 11.2 77 24 ABK61114 SELEX process nucl  
c 128 28 11.2 78 14 AAQ52392 Template RNA used  
c 129 28 11.2 79 21 AAA12100 T. brucei trypanos  
c 130 28 11.2 80 24 AAL48343 Cytohesin binding  
c 131 28 11.2 82 20 AAX78164 Selex procedure an  
c 132 28 11.2 83 20 AAX78162 Selex procedure ta  
c 133 28 11.2 83 20 AAX78168 T7 RNA polymerase  
c 134 28 11.2 86 22 AAD10615 JH101 oligo used i  
c 135 28 11.2 87 15 AAQ63023 Template used in S  
c 136 28 11.2 87 16 AAQ89175 VEGF RNA high affi  
137 28 11.2 87 17 AAT42819 Oligonucleotide 40  
138 28 11.2 87 17 AAT28376 40N8 random sequen  
139 28 11.2 87 17 AAT28378 30N1 random sequen  
140 28 11.2 87 18 AAT93776 Rous sarcoma virus  
c 141 28 11.2 87 18 AAT84602 DNA template for s  
142 28 11.2 87 18 AAT87285 40N ssDNA template  
143 28 11.2 87 18 AAT87173 40N8 ssDNA templat  
c 144 28 11.2 87 18 AAT79123 SELEX template use  
145 28 11.2 87 18 AAT78661 40N template, for  
c 146 28 11.2 87 18 AAT65425 Transforming growt  
147 28 11.2 87 18 AAT65428 Transforming growt  
148 28 11.2 87 19 AAV41761 Random sequence RN  
149 28 11.2 87 19 AAV43312 Randomised oligonu  
150 28 11.2 87 20 AAX85097 Human fibrin ligan  
151 28 11.2 87 20 AAX01789 Oligonucleotide 40  
152 28 11.2 87 21 AAA13670 40N8 RNA pool rand  
153 28 11.2 87 22 AAF73759 HGF nucleic acid 1  
154 28 11.2 87 22 AAF73760 HGF nucleic acid 1

c 155 28 11.2 87 22 AAC84734 Nucleotide sequenc  
156 28 11.2 90 19 AAV39807 Anti-E4 RNA oligon  
157 28 11.2 90 24 ABK13906 Template DNA used  
c 158 28 11.2 91 22 AAF16661 DAMP specific apta  
159 28 11.2 93 14 AAQ39251 Platelet adhesion  
160 28 11.2 93 16 AAQ79694 Antisense oligonuc  
161 28 11.2 93 16 AAQ79087 Oligonucleotide en  
162 28 11.2 93 19 AAV35010 Human endothelin-b  
163 28 11.2 93 21 AAA27010 Oligonucleotide fo  
c 164 28 11.2 94 18 AAT94526 Gene library codin  
c 165 28 11.2 94 20 AAX15131 Coding sequence of  
166 28 11.2 94 22 AAF73455 Hepatocyte growth  
167 28 11.2 95 21 AAA93771 Adaptor used in me  
168 28 11.2 96 18 AAT65435 Platelet derived g  
169 28 11.2 96 20 AAX87036 Starting RNA used  
170 28 11.2 97 18 AAT58049 Template 50N8 for  
171 28 11.2 100 16 AAQ92421 Human HLA-DRB frag  
172 28 11.2 100 20 AAX78167 T7 RNA polymerase  
173 28 11.2 104 19 AAV41760 Synthetic DNA temp  
174 28 11.2 104 19 AAV43311 Randomised oligonu  
175 28 11.2 104 22 AAF73640 HGF nucleic acid 1  
176 28 11.2 104 24 ABK31550 DNA template for c  
177 28 11.2 104 25 ABX80491 Nucleic acid ligan  
c 178 28 11.2 107 16 AAT06076 Template sequence  
179 28 11.2 107 16 AAT06079 RNA template from  
c 180 28 11.2 107 21 AAA48470 Termamyl-like alph  
c 181 28 11.2 111 18 AAV77549 Staphylococcus aur  
c 182 28 11.2 113 24 ABQ82152 Oligonucleotide li  
c 183 28 11.2 113 24 ABS52652 RNA aptamer oligon  
c 184 28 11.2 114 24 AAS20468 Library oligonucle  
c 185 28 11.2 118 18 AAV75833 Staphylococcus aur  
c 186 28 11.2 119 14 AAQ48613 Synthetic antibody  
c 187 28 11.2 123 24 ABA94828 Nucleotide sequenc  
188 28 11.2 124 24 ABA94841 Nucleotide sequenc  
189 28 11.2 147 20 AAX01793 Oligonucleotide 10  
190 28 11.2 147 21 AAA13674 147 nucleotide 100  
c 191 28 11.2 162 18 AAV75660 Staphylococcus aur  
c 192 28 11.2 204 18 AAV77458 Staphylococcus aur  
c 193 28 11.2 217 24 ABK93423 Human breast speci  
194 28 11.2 233 24 AAD28249 Human pancreatic t  
195 28 11.2 236 24 ABL74465 Corn tassell-derive  
196 28 11.2 251 18 AAV78865 Staphylococcus aur  
197 28 11.2 281 24 ABN87704 Human prostate spe  
198 28 11.2 283 25 ABX82525 Corn ear-derived p  
199 28 11.2 284 24 ABL72867 Corn tassell-derive  
c 200 28 11.2 285 22 AAL08943 Human breast cance  
c 201 28 11.2 287 25 ABX87111 Corn ear-derived p  
202 28 11.2 311 23 ABV24993 Human prostate exp  
c 203 28 11.2 322 23 ABV25624 Human prostate exp  
c 204 28 11.2 326 18 AAV77421 Staphylococcus aur  
c 205 28 11.2 330 24 ABT03316 Ovary cell-specific  
206 28 11.2 337 12 AAQ12093 pregnancy-specific  
207 28 11.2 339 24 AAL39963 Lung-specific nucl  
208 28 11.2 341 23 AAS82087 DNA encoding novel  
209 28 11.2 351 18 AAV78652 Staphylococcus aur  
c 210 28 11.2 351 18 AAV78389 Staphylococcus aur  
c 211 28 11.2 362 22 AAI84424 Human polynucleoti  
212 28 11.2 368 22 AAL08035 Human breast cance  
c 213 28 11.2 368 22 AAL08035 Human breast cance  
c 214 28 11.2 373 21 AAA98496 Vicuna PTEN/MMAC1  
c 215 28 11.2 374 22 AAL11395 Human breast cance  
c 216 28 11.2 382 22 AAS43337 DNA encoding novel  
c 217 28 11.2 389 18 AAV78201 Staphylococcus aur  
c 218 28 11.2 390 24 ABQ73825 Human colon specif  
c 219 28 11.2 391 22 AAD17399 Human bone marrow  
220 28 11.2 398 23 AAS65727 DNA encoding novel  
221 28 11.2 398 23 AAS91583 DNA encoding novel  
c 222 28 11.2 398 25 ABZ18330 Group III cDNA can  
c 223 28 11.2 399 18 AAV77682 Staphylococcus aur  
c 224 28 11.2 400 18 AAV78203 Staphylococcus aur  
c 225 28 11.2 400 18 AAV78167 Staphylococcus aur  
c 226 28 11.2 400 18 AAV78076 Staphylococcus aur  
c 227 28 11.2 400 18 AAV77945 Staphylococcus aur



228	28	11.2	400	18	AAV77258	Staphylococcus aur
229	28	11.2	407	23	AAS75914	DNA encoding novel
230	28	11.2	408	23	AAS65726	DNA encoding novel
231	28	11.2	408	23	AAS91582	DNA encoding novel
232	28	11.2	412	23	AAS69064	DNA encoding novel
233	28	11.2	414	18	AAV75283	Staphylococcus aur
234	28	11.2	418	22	AAAL11525	Human breast cance
235	28	11.2	420	22	AAI831188	Human polynucleoti
236	28	11.2	423	22	AAS58918	Human cancer relat
237	28	11.2	423	23	AAS82916	DNA encoding novel
238	28	11.2	429	22	AAS58915	Human cancer relat
239	28	11.2	432	22	AAAL08519	Human breast cance
c 240	28	11.2	440	24	ABK933480	Human breast speci
c 241	28	11.2	441	25	ABZ18254	Group III cDNA can
c 242	28	11.2	450	23	AAS88231	DNA encoding novel
243	28	11.2	459	20	AAV84299	Wheat geminivirus
244	28	11.2	462	20	AAV84300	Wheat geminivirus
245	28	11.2	464	23	AAS68866	DNA encoding novel
c 246	28	11.2	464	25	ACA57175	Human adipocyte Se
247	28	11.2	470	22	AAI92703	Human polynucleoti
c 248	28	11.2	471	22	AAAL10724	Human breast cance
c 249	28	11.2	476	18	AAV77886	Staphylococcus aur
250	28	11.2	477	23	AAS91524	DNA encoding novel
c 251	28	11.2	481	22	AAAL11459	Human breast cance
252	28	11.2	483	22	AAAL11282	Human breast cance
253	28	11.2	491	22	AAI89562	Human polynucleoti
254	28	11.2	495	18	AAV75525	Staphylococcus aur
c 255	28	11.2	498	23	AAS72533	DNA encoding novel
c 256	28	11.2	498	23	AAS72567	DNA encoding novel
257	28	11.2	498	23	AAS81004	DNA encoding novel
c 258	28	11.2	517	22	AAH72557	Human cervical can
259	28	11.2	525	25	ABZ20427	Oncofaetal cDNA se
260	28	11.2	531	22	AAK32668	Human bone marrow
261	28	11.2	531	22	AAI38483	Probe #7169 used t
262	28	11.2	531	23	ABS32385	Human liver single
263	28	11.2	531	24	ABS07462	Human genome-deriv
c 264	28	11.2	548	22	AAAL08030	Human breast cance
265	28	11.2	574	18	AAV74886	Staphylococcus aur
266	28	11.2	588	23	ABV60736	Human prostate exp
267	28	11.2	590	22	AAAL07880	Human breast cance
c 268	28	11.2	608	23	ABV50405	Human prostate exp
269	28	11.2	609	24	ABK92487	Human prostate spe
c 270	28	11.2	617	24	ABN89007	Human prostate spe
271	28	11.2	635	22	AAI80602	Human polynucleoti
c 272	28	11.2	641	18	AAV75788	Staphylococcus aur
273	28	11.2	654	18	AAV75491	Staphylococcus aur
274	28	11.2	670	19	AAV43797	Sequence used in t
c 275	28	11.2	670	19	AAV43797	Sequence used in t
c 276	28	11.2	672	25	ABZ18301	Group III cDNA can
c 277	28	11.2	682	18	AAV74751	Staphylococcus aur
278	28	11.2	693	22	AAAL09069	Human breast cance
c 279	28	11.2	693	22	AAAL09069	Human breast cance
280	28	11.2	738	14	AAQ48606	Sequence encoding
281	28	11.2	740	24	ABQ68262	Listeria monocytog
282	28	11.2	740	24	ABQ70070	Listeria monocytog
283	28	11.2	756	24	AAAL39964	Lung-specific nucl
284	28	11.2	760	18	AAV75133	Staphylococcus aur
285	28	11.2	760	22	AAI93329	Human polynucleoti
286	28	11.2	764	22	AAI92185	Human polynucleoti
287	28	11.2	774	24	ABQ70962	Listeria monocytog
288	28	11.2	780	24	ABK14447	Modified version o
c 289	28	11.2	784	22	AAAL10510	Human breast cance
c 290	28	11.2	821	22	AAH94043	Human foetal cDNA,
c 291	28	11.2	835	22	AAF933182	cDNA encoding SRT
c 292	28	11.2	840	24	ABK47980	Human small induci
293	28	11.2	883	23	ABV19680	Human prostate exp
c 294	28	11.2	886	18	AAV74856	Staphylococcus aur
c 295	28	11.2	914	22	AAI85445	Human polynucleoti
296	28	11.2	918	24	ABT03398	Ovary cell-specifi
c 297	28	11.2	919	22	AAI87811	Human polynucleoti
298	28	11.2	951	24	ABQ70259	Listeria monocytog
299	28	11.2	958	22	AAI88868	Human polynucleoti
300	28	11.2	960	20	AAZ16277	Human gene express

301	28	11.2	963	24	ABZ43156	Human GPCR polynuc
c 302	28	11.2	963	24	ABZ43156	Human GPCR polynuc
303	28	11.2	972	23	AAS66748	DNA encoding novel
c 304	28	11.2	986	25	ABZ18486	Group III cDNA can
c 305	28	11.2	1003	18	AAV74634	Staphylococcus aur
306	28	11.2	1010	22	AAI89570	Human polynucleoti
307	28	11.2	1021	18	AAV74325	Staphylococcus aur
c 308	28	11.2	1060	18	AAV74766	Staphylococcus aur
c 309	28	11.2	1071	24	ABZ43147	Human GPCR polynuc
310	28	11.2	1072	24	ABK92515	Human prostate spe
311	28	11.2	1090	24	ABK92516	Human prostate spe
312	28	11.2	1126	11	AAQ06974	Human follicle-sti
c 313	28	11.2	1134	24	ABT07897	Human lung specifi
c 314	28	11.2	1139	23	AAS87665	DNA encoding novel
c 315	28	11.2	1145	18	AAV75088	Staphylococcus aur
316	28	11.2	1157	24	ABK53293	Human eosinophil-m
317	28	11.2	1166	20	AAK88570	Human chromosome 1
318	28	11.2	1191	25	ABZ18419	Group III cDNA can
319	28	11.2	1200	24	ABK72649	Modified DNA encod
c 320	28	11.2	1242	18	AAV74901	Staphylococcus aur
c 321	28	11.2	1257	18	AAV75030	Staphylococcus aur
c 322	28	11.2	1260	24	ABL52277	Human modified PHK
323	28	11.2	1280	22	AAF80542	Receptor #30 parti
c 324	28	11.2	1308	18	AAV74387	Staphylococcus aur
325	28	11.2	1312	18	AAV74494	Staphylococcus aur
326	28	11.2	1320	25	AAD51674	Human cytochrome P
c 327	28	11.2	1320	25	AAD51674	Human cytochrome P
c 328	28	11.2	1354	25	ABZ18320	Group III cDNA can
329	28	11.2	1373	18	AAV74820	Staphylococcus aur
330	28	11.2	1461	16	AAAT30576	Leuconostoc lactis
c 331	28	11.2	1490	24	ABL54570	Rhodospirillum rDN
332	28	11.2	1500	24	ABK14142	Human aminolevulin
c 333	28	11.2	1544	24	ABS71615	Legionella pneumop
c 334	28	11.2	1560	24	AAD43682	Human interleukin
335	28	11.2	1609	24	AAS94861	Human DNA sequence
c 336	28	11.2	1680	24	ABK52231	Human CYP27A1 modi
c 337	28	11.2	1683	22	AAC66921	Human amyloid prec
338	28	11.2	1782	16	AAT03251	Pseudomonas mesoac
c 339	28	11.2	1788	18	AAV74701	Staphylococcus aur
c 340	28	11.2	1801	23	ABV21121	Human prostate exp
c 341	28	11.2	1801	23	ABV23347	Human prostate exp
c 342	28	11.2	1801	23	ABV25696	Human prostate exp
c 343	28	11.2	1801	23	ABV26963	Human prostate exp
344	28	11.2	1812	12	AAQ11071	Chromosomal HindII
345	28	11.2	1814	18	AAV74769	Staphylococcus aur
346	28	11.2	1816	18	AAV74662	Staphylococcus aur
347	28	11.2	1910	24	ABZ35468	Human gene express
c 348	28	11.2	1941	24	ABZ35435	Human gene express
349	28	11.2	1972	22	AAK52691	Human polynucleoti
350	28	11.2	1975	22	AAH89873	Human bone marrow
c 351	28	11.2	1984	18	AAV74450	Staphylococcus aur
352	28	11.2	2040	24	ABK11513	Human beta-3-adren
353	28	11.2	2141	22	AAH75061	Nucleotide sequenc
c 354	28	11.2	2146	25	ACA03962	cDNA downregulated
c 355	28	11.2	2148	24	AAS94996	Human DNA sequence
356	28	11.2	2201	24	ABZ35346	Human gene express
c 357	28	11.2	2209	24	ABK14301	DNA encoding proli
c 358	28	11.2	2343	18	AAV74468	Staphylococcus aur
c 359	28	11.2	2365	18	AAV74406	Staphylococcus aur
360	28	11.2	2366	24	ABK14302	DNA encoding trp s
361	28	11.2	2400	24	ABK50461	Human caspase 5, a
c 362	28	11.2	2400	24	ABK50461	Human caspase 5, a
363	28	11.2	2409	21	AAZ30341	Partial sequence o
c 364	28	11.2	2518	18	AAV74680	Staphylococcus aur
365	28	11.2	2549	18	AAV74936	Staphylococcus aur
366	28	11.2	2569	18	AAV74385	Staphylococcus aur
367	28	11.2	2574	18	AAV74752	Staphylococcus aur
c 368	28	11.2	2822	23	ABV22239	Human prostate exp
c 369	28	11.2	2822	23	ABV23675	Human prostate exp
c 370	28	11.2	2822	23	ABV28077	Human prostate exp
c 371	28	11.2	2822	23	ABV29539	Human prostate exp
372	28	11.2	2848	24	ABZ35045	Human gene express
c 373	28	11.2	2980	24	ABZ35345	Human gene express

374	28	11.2	3083	20	AAx58284	Human methylthioad	447	28	11.2	19806	24	ABN89476	Human dehydrogenas
375	28	11.2	3083	25	ABX10818	DNA encoding rat m	c 449	28	11.2	21990	18	ABK50071	Human Cyp 4A11 gen
376	28	11.2	3176	18	AAV74726	Staphylococcus aur	c 449	28	11.2	22243	18	AAV74475	Staphylococcus aur
377	28	11.2	3240	24	ABL52076	Human SLC18A2 modi	450	28	11.2	22884	24	ABQ99649	Human membrane spa
378	28	11.2	3240	24	ABL52076	Human SLC18A2 modi	c 451	28	11.2	23439	18	AAV74349	Staphylococcus aur
379	28	11.2	3521	14	AAQ41230	Gene encoding majo	452	28	11.2	27754	24	ABQ72998	Human transporter
380	28	11.2	3600	24	ABK47911	Human B-Factor Pro	453	28	11.2	30246	18	AAV74367	Staphylococcus aur
381	28	11.2	3675	24	ABK12468	Plasmid vector pGX	454	28	11.2	31766	24	AAAL50687	Human sulphate tra
382	28	11.2	3733	24	AAS94816	Human DNA sequence	455	28	11.2	31766	24	AAD22781	Human sulphate tra
383	28	11.2	3821	18	AAV74615	Staphylococcus aur	456	28	11.2	31814	25	ADA47150	Human Ras-like pro
384	28	11.2	3963	23	ABV25520	Human prostate exp	457	28	11.2	32480	24	ABA94267	Adenovirus related
385	28	11.2	4021	25	ACA03936	cDNA downregulated	458	28	11.2	34337	24	ABL55857	Human GABA transpo
386	28	11.2	4021	25	ABX62924	Human activated T	459	28	11.2	46050	25	ABX13974	Human Ras-like pro
387	28	11.2	4029	18	AAV74612	Staphylococcus aur	c 460	28	11.2	62488	24	ADA44981	Human EMR1 splice
388	28	11.2	4034	24	AAS94906	Human DNA sequence	c 461	28	11.2	67087	21	AAF22280	BAC containing rep
389	28	11.2	4035	24	ABZ35238	Human gene express	462	28	11.2	69327	24	ABS55821	Human transporter
390	28	11.2	4151	23	ABV24466	Human prostate exp	c 463	28	11.2	73544	25	ABS56296	Human transporter
391	28	11.2	4394	24	ABZ35513	Human gene express	c 464	28	11.2	95223	21	AAF22282	BAC containing rep
392	28	11.2	4467	22	AAC85085	Atherosclerosis-as	465	28	11.2	114693	25	AAD48308	Human transporter
393	28	11.2	4549	18	AAV74485	Staphylococcus aur	c 466	28	11.2	121001	21	AAF22284	BAC containing rep
394	28	11.2	4557	18	AAV74652	Staphylococcus aur	c 467	28	11.2	215980	24	AAAL38337	Complementary stra
395	28	11.2	4576	25	ABX63703	Human cDNA #703 di	c 468	28	11.2	249999	25	ABZ80229	Human tramdorin ge
396	28	11.2	4669	18	AAV74443	Staphylococcus aur	c 469	28	11.2	326014	24	ABK89296	Human gene for nov
397	28	11.2	4721	18	AAV74545	Staphylococcus aur	470	28	11.2	567571	25	AAD53224	Human chromosome 3
398	28	11.2	4733	18	AAV74744	Staphylococcus aur	c 471	28	11.2	567571	25	AAD53224	Human chromosome 3
399	28	11.2	4832	18	AAV74500	Staphylococcus aur	c 472	28	11.2	786431	24	ABQ74964	Human kinase prote
400	28	11.2	4854	18	AAV74417	Staphylococcus aur	c 473	27	10.8	39	19	AAV44493	Cleavage site of h
401	28	11.2	5024	24	AAS94874	Human DNA sequence	c 474	27	10.8	39	19	AAV44494	Cleavage site of h
402	28	11.2	5097	22	AAH57447	Human lung cell ep	475	27	10.8	40	21	AAC70152	EcoRI/PstI-digeste
403	28	11.2	5301	24	AAS94869	Human DNA sequence	c 476	27	10.8	48	24	AAD40013	Seleno-cysteine in
404	28	11.2	5445	18	AAV74384	Staphylococcus aur	477	27	10.8	61	21	AAC70148	EcoRI/PstI DNA str
405	28	11.2	5532	18	AAV74841	Staphylococcus aur	c 478	27	10.8	61	21	AAC70149	EcoRI/PstI DNA str
406	28	11.2	5763	18	AAV74816	Staphylococcus aur	479	27	10.8	66	18	AAV79491	Staphylococcus aur
407	28	11.2	5804	18	AAV74560	Staphylococcus aur	480	27	10.8	66	22	AA508440	A random oligonucl
408	28	11.2	5895	18	AAV74312	Staphylococcus aur	481	27	10.8	70	24	ABL57073	Molecular beacon r
409	28	11.2	5924	18	AAV74441	Staphylococcus aur	482	27	10.8	72	13	AAQ21832	Randomising oligon
410	28	11.2	5966	18	AAV74333	Staphylococcus aur	483	27	10.8	72	14	AAQ36857	PCR primer for 5'
411	28	11.2	6591	18	AAV77425	Staphylococcus aur	484	27	10.8	72	19	AAV39804	Anti-E4 RNA oligon
412	28	11.2	6637	24	AAS94962	Human DNA sequence	485	27	10.8	72	20	AAV64954	Mouse histone H2B
413	28	11.2	6876	18	AAV74497	Staphylococcus aur	486	27	10.8	72	22	AAF76908	Sequence containin
414	28	11.2	6876	18	AAV74497	Staphylococcus aur	487	27	10.8	72	24	AAI72773	Oligo #5 for cloni
415	28	11.2	6970	25	ABZ24594	Mouse ovary-epicif	488	27	10.8	72	24	ABA01319	pseudoknot oligonu
416	28	11.2	7953	18	AAV74463	Staphylococcus aur	489	27	10.8	72	24	ABK13903	DNA oligonucleotid
417	28	11.2	7965	18	AAV74632	Staphylococcus aur	c 490	27	10.8	73	17	AAV71327	Red blood cell gho
418	28	11.2	8339	18	AAV74486	Staphylococcus aur	c 491	27	10.8	73	19	AAV39808	Anti-E4 RNA oligon
419	28	11.2	8668	14	AAQ50433	Partial human geno	c 492	27	10.8	73	24	ABK13907	RNA transcript use
420	28	11.2	8779	18	AAV74369	Staphylococcus aur	c 493	27	10.8	75	16	AAQ98305	SELEX template mol
421	28	11.2	9179	18	AAV74411	Staphylococcus aur	c 494	27	10.8	76	16	AAQ98396	Template molecule
422	28	11.2	9280	18	AAV74442	Staphylococcus aur	c 495	27	10.8	76	16	AAQ89163	VEGF RNA high affi
423	28	11.2	9310	18	AAV74627	Staphylococcus aur	496	27	10.8	76	21	AAZ39846	76mer library form
424	28	11.2	9834	18	AAV74348	Staphylococcus aur	c 497	27	10.8	76	22	AAF70633	SELEX experiment s
425	28	11.2	10182	18	AAV74427	Staphylococcus aur	c 498	27	10.8	77	15	AAQ63025	Template used in s
426	28	11.2	10758	18	AAV74532	Staphylococcus aur	c 499	27	10.8	77	16	AAV73196	Template sequence
427	28	11.2	11466	18	AAV74755	Staphylococcus aur	c 500	27	10.8	77	16	AAQ89172	VEGF RNA high affi
428	28	11.2	11544	22	AAC91455	celZ integration v	c 501	27	10.8	77	17	AAV79615	Generic nucleic ac
429	28	11.2	11544	24	ABK13045	celZ integration v	c 502	27	10.8	77	17	AAV07689	First cycle start
430	28	11.2	11544	24	ABK13045	celZ integration v	c 503	27	10.8	77	18	AAV00778	Template for isola
431	28	11.2	11992	20	AAZ24729	Mouse amyloid prec	c 504	27	10.8	77	18	AAV87305	30N ssDNA template
432	28	11.2	11992	20	AAZ24729	Mouse amyloid prec	c 505	27	10.8	77	19	AAV14559	SELEX template for
433	28	11.2	12494	24	ABA01438	Streptococcus ther	c 506	27	10.8	77	20	AAV01791	Oligonucleotide 30
434	28	11.2	12718	24	ABK52229	cDNA encoding huma	c 507	27	10.8	77	20	AAV79638	Starting RNA seque
435	28	11.2	13059	18	AAV74531	Staphylococcus aur	c 508	27	10.8	77	21	AAA92738	HSV-1 DNA polymera
436	28	11.2	13182	25	ABX15028	Human gene encodin	c 509	27	10.8	77	21	AAA13672	GMPS-RNA molecule
437	28	11.2	13856	18	AAV74342	Staphylococcus aur	c 510	27	10.8	77	21	AAZ52749	Randomised nucleot
438	28	11.2	15249	18	AAV74413	Staphylococcus aur	c 511	27	10.8	77	22	AAF73456	Hepatocyte growth
439	28	11.2	15347	24	ABA01439	Streptococcus ther	c 512	27	10.8	77	22	AAF70539	SELEX experiment o
440	28	11.2	16110	24	ABA01437	Streptococcus ther	c 513	27	10.8	77	24	ABK61114	SELEX process nucl
441	28	11.2	16592	18	AAV74364	Staphylococcus aur	c 514	27	10.8	78	14	AAQ52392	Template RNA used
442	28	11.2	16826	18	AAV74357	Staphylococcus aur	c 515	27	10.8	78	19	AAV16706	Primer of the inve
443	28	11.2	16826	18	AAV74357	Staphylococcus aur	c 516	27	10.8	78	21	AAZ92120	Primer used to amp
444	28	11.2	18355	18	AAV74378	Staphylococcus aur	517	27	10.8	82	20	AAV78164	Selex procedure an
445	28	11.2	18613	18	AAV74423	Staphylococcus aur	518	27	10.8	82	24	ABQ81252	Randomised oligonu
446	28	11.2	19738	24	ABA01436	Streptococcus ther	519	27	10.8	83	20	AAV78162	Selex procedure ta

C 520	27	10.8	83	20	AAx78168	T7 RNA polymerase	593	27	10.8	131	23	ABL41605	Nucleotide sequenc
C 521	27	10.8	85	18	AAV76406	Staphylococcus aur	594	27	10.8	133	24	ABL40278	Anti-DNA antibody
522	27	10.8	86	22	AAAD10615	JH101 oligo used i	C 595	27	10.8	137	18	AAV79044	Staphylococcus aur
523	27	10.8	87	15	AAQ63023	Template used in S	596	27	10.8	138	18	AAV77147	Staphylococcus aur
524	27	10.8	87	16	AAQ89175	VEGF RNA high affi	C 597	27	10.8	139	24	ABA01325	Pseudoknot oligonu
C 525	27	10.8	87	17	AAQ42819	Oligonucleotide 40	598	27	10.8	141	18	AAV79206	Staphylococcus aur
C 526	27	10.8	87	17	AAT28376	40N8 random sequen	599	27	10.8	141	18	AAT79487	Adenosine or adeno
C 527	27	10.8	87	17	AAT28378	30N1 random sequen	C 600	27	10.8	142	18	AAT79486	Adenosine or adeno
C 528	27	10.8	87	18	AAT93776	Rous sarcoma virus	601	27	10.8	145	18	AAV75966	Staphylococcus aur
C 529	27	10.8	87	18	AAT84602	DNA template for s	C 602	27	10.8	147	18	AAV75637	Staphylococcus aur
C 530	27	10.8	87	18	AAT87285	40N ssDNA template	C 603	27	10.8	147	20	AAx01793	Oligonucleotide 10
C 531	27	10.8	87	18	AAT87173	40N8 ssDNA templat	604	27	10.8	147	20	AAx01794	Oligonucleotide 10
532	27	10.8	87	18	AAT79123	SELEX template use	C 605	27	10.8	147	20	AAx01794	Oligonucleotide 10
C 533	27	10.8	87	18	AAT78661	40N template, for	C 606	27	10.8	147	21	AAAL3674	147 nucleotide 100
534	27	10.8	87	18	AAT65425	Transforming growt	607	27	10.8	147	21	AAAL3675	147 nucleotide 100
C 535	27	10.8	87	18	AAT65428	Transforming growt	C 608	27	10.8	147	21	AAAL3675	147 nucleotide 100
C 536	27	10.8	87	19	AAV41761	Random sequence RN	C 609	27	10.8	148	18	AAV77593	Staphylococcus aur
C 537	27	10.8	87	19	AAV43312	Randomised oligonu	610	27	10.8	156	20	AAx88213	Oligonucleotide pr
C 538	27	10.8	87	20	AAx01789	Human fibrin ligan	C 611	27	10.8	156	20	AAx88213	Oligonucleotide pr
C 539	27	10.8	87	20	AAx01789	Oligonucleotide 40	C 612	27	10.8	165	4	AAAN30314	Sequence of portio
C 540	27	10.8	87	21	AAAL3670	40N8 RNA pool rand	C 613	27	10.8	165	5	AAAN40294	Sequence of portio
C 541	27	10.8	87	22	AAF73759	HGF nucleic acid 1	C 614	27	10.8	165	18	AAV75693	Staphylococcus aur
C 542	27	10.8	87	22	AAF73760	HGF nucleic acid 1	C 615	27	10.8	171	21	AAZ56692	Red clover necroti
543	27	10.8	87	22	AAC84734	Nucleotide sequenc	616	27	10.8	179	22	AAI84781	Human polynucleoti
544	27	10.8	88	18	AAV77761	Staphylococcus aur	C 617	27	10.8	193	24	ABQ73532	HPV-PTM related ol
C 545	27	10.8	90	19	AAV39807	Anti-E4 RNA oligon	C 618	27	10.8	199	19	AAV23176	Saccharomyces cere
C 546	27	10.8	90	19	AAV11329	pDR-47 D-Arginine	619	27	10.8	199	25	ACA56323	Human signalling p
C 547	27	10.8	90	24	ABK13906	Template DNA used	620	27	10.8	208	18	AAT79488	Adenosine or adeno
548	27	10.8	92	16	AAQ83452	Template oligonucl	C 621	27	10.8	208	18	AAT79488	Adenosine or adeno
549	27	10.8	92	18	AAT36331	Feline immunodefic	622	27	10.8	214	8	AAAN71331	Exon 3 human chrom
C 550	27	10.8	92	18	AAT36331	Feline immunodefic	C 623	27	10.8	215	24	ABK92416	Human prostate spe
551	27	10.8	92	20	AAx88045	Ku protein binding	624	27	10.8	222	6	AAAN50752	Sequence of the hu
C 552	27	10.8	92	20	AAx88045	Ku protein binding	C 625	27	10.8	222	6	AAAN50752	Sequence of the hu
553	27	10.8	92	24	AAD30602	(AT)4-40N18-(A)8,	C 626	27	10.8	231	24	ABA01284	HIV-1 oligonucleot
C 554	27	10.8	92	24	AAD30602	(AT)4-40N18-(A)8,	C 627	27	10.8	233	24	ABL75970	Corn tassell-derive
C 555	27	10.8	94	22	AAF73455	Hepatocyte growth	C 628	27	10.8	235	22	AAAL10146	Human breast cance
C 556	27	10.8	96	18	AAT65435	Platelet derived g	629	27	10.8	236	25	ABQ82915	Human lung specifi
C 557	27	10.8	96	20	AAx87036	Starting RNA used	630	27	10.8	237	22	AAAL08493	Human breast cance
C 558	27	10.8	97	18	AAT58049	Template 50N8 for	C 631	27	10.8	238	23	ABV60620	Human prostate exp
C 559	27	10.8	97	24	AAAL45385	Ion-dependent deox	632	27	10.8	240	22	AAAL08779	Human breast cance
560	27	10.8	97	24	AAAL45390	RNA-cleaving deox	C 633	27	10.8	247	24	ABL71831	Corn tassell-derive
561	27	10.8	99	19	AAV60453	Oligonucleotide us	634	27	10.8	249	18	AAV78931	Staphylococcus aur
562	27	10.8	99	24	AAAL48342	Cytohesin PCR prim	635	27	10.8	250	18	AAV75569	Staphylococcus aur
C 563	27	10.8	99	24	ABA01289	SECIS element #4.	C 636	27	10.8	250	22	AAAL08845	Human breast cance
C 564	27	10.8	100	18	AAV06063	DNA template for u	637	27	10.8	252	25	ABX83328	Corn ear-derived p
C 565	27	10.8	100	20	AAZ23606	Template primer DN	C 638	27	10.8	264	8	AAAN71333	Exon 5 human chrom
C 566	27	10.8	100	20	AAx78167	T7 RNA polymerase	639	27	10.8	265	25	ABX81751	Corn ear-derived p
567	27	10.8	101	16	AAQ93245	Random RNA templat	640	27	10.8	268	25	ABX82644	Corn ear-derived p
C 568	27	10.8	102	18	AAV77044	Staphylococcus aur	C 641	27	10.8	269	18	AAV78808	Staphylococcus aur
569	27	10.8	103	24	ABL51893	Nucleic acid senso	C 642	27	10.8	269	18	AAV75643	Staphylococcus aur
C 570	27	10.8	104	18	AAV79158	Staphylococcus aur	C 643	27	10.8	270	22	AAI89657	Human polynucleoti
C 571	27	10.8	104	19	AAV41760	Synthetic DNA temp	C 644	27	10.8	270	22	AAI90145	Human polynucleoti
C 572	27	10.8	104	19	AAV43311	Randomised oligonu	645	27	10.8	271	25	ABX81918	Corn ear-derived p
C 573	27	10.8	104	22	AAF73640	HGF nucleic acid 1	646	27	10.8	275	22	AAI84880	Human polynucleoti
C 574	27	10.8	104	24	ABK31550	DNA template for c	647	27	10.8	279	25	ABX84949	Corn ear-derived p
C 575	27	10.8	104	25	ABX80491	Nucleic acid ligan	648	27	10.8	282	24	ABL74016	Corn tassell-derive
576	27	10.8	107	16	AAT06076	Template sequence	649	27	10.8	282	25	ABX83778	Corn ear-derived p
C 577	27	10.8	107	16	AAT06079	RNA template from	C 650	27	10.8	282	25	ABX85720	Corn ear-derived p
578	27	10.8	107	17	AAT34901	Single stranded DN	C 651	27	10.8	282	25	ABV93939	Human colon specif
579	27	10.8	107	20	AAV82944	Enzymatic DNA 107m	C 652	27	10.8	284	24	ABN87653	Human prostate spe
580	27	10.8	107	21	AAA92244	Synthetic oligomer	653	27	10.8	285	22	AAAL08943	Human breast cance
581	27	10.8	113	24	ABQ82152	Oligonucleotide li	C 654	27	10.8	285	23	ABV19903	Human prostate exp
582	27	10.8	113	24	ABS52652	RNA aptamer oligon	655	27	10.8	290	24	ABL71025	Corn tassell-derive
583	27	10.8	114	18	AAV75798	Staphylococcus aur	C 657	27	10.8	292	25	ABX82351	Corn ear-derived p
584	27	10.8	114	24	AAS20468	Library oligonucle	C 658	27	10.8	296	22	AAI81570	Human polynucleoti
C 585	27	10.8	116	24	AAAL43035	Regulatable, catal	659	27	10.8	296	23	AAS85636	DNA encoding novel
586	27	10.8	118	18	AAV75666	Staphylococcus aur	660	27	10.8	297	22	AAAL08856	Human breast cance
C 587	27	10.8	123	18	AAV77224	Staphylococcus aur	C 661	27	10.8	299	20	AAx98276	Human cancer cell
C 588	27	10.8	124	21	AAZ44035	Construct 5' CAEV-	662	27	10.8	299	22	AAI91740	Human polynucleoti
C 589	27	10.8	124	24	ABA94841	Nucleotide sequenc	663	27	10.8	303	22	AAAL25388	Human breast cance
590	27	10.8	130	18	AAV77204	Staphylococcus aur	C 664	27	10.8	303	22	AAAL25388	Human breast cance
591	27	10.8	130	23	ABL52908	Sialyl l lewis-rela	C 665	27	10.8	303	25	ABX87363	Corn ear-derived p
592	27	10.8	130	23	ABL54860	Cholesterol specif							



666 AAL07642 304 22 Human breast cance  
c 667 AAL07642 304 22 Human breast cance  
668 ABX87415 305 25 Corn ear-derived p  
669 AAV75426 317 18 Staphylococcus aur  
c 670 AAV75749 321 18 Staphylococcus aur  
c 671 AAV75479 321 18 Staphylococcus aur  
c 672 AAV78594 324 18 Staphylococcus aur  
673 AAI93664 324 22 Human polynucleoti  
c 674 AAS68328 324 23 DNA encoding novel  
c 675 AAV78640 325 18 Staphylococcus aur  
c 676 AAV78835 326 18 Staphylococcus aur  
677 AAV75476 327 18 Staphylococcus aur  
678 AAV78701 333 18 Staphylococcus aur  
c 679 AAV75337 333 18 Staphylococcus aur  
680 AAI87593 334 22 Human polynucleoti  
681 AAQ70086 336 15 DNA encoding MAb 1  
c 682 ABV23161 337 23 Human prostate exp  
c 683 ABV29001 337 23 Human prostate exp  
c 684 AAS76170 337 23 DNA encoding novel  
c 685 AAV78601 338 18 Staphylococcus aur  
686 AAV78526 338 18 Staphylococcus aur  
c 687 ABV54264 338 23 Human prostate exp  
c 688 AAV77402 340 18 Staphylococcus aur  
c 689 AAL08552 343 22 Human breast cance  
c 690 AAZ21044 345 20 Human NEMM antibod  
c 691 ABK12526 345 24 DNA template for c  
692 AAV78550 348 18 Staphylococcus aur  
693 ABV30283 350 23 Human prostate exp  
c 694 AAV76126 351 18 Staphylococcus aur  
c 695 AAS93514 352 23 DNA encoding novel  
696 ABZ18556 354 25 Group III cDNA can  
c 697 AAL11352 357 22 Human breast cance  
698 AAS77752 359 23 DNA encoding novel  
c 699 AAS78872 359 23 DNA encoding novel  
700 ABK12100 360 24 Human interferon-g  
701 ABV76206 360 25 Nicotinamide N-met  
c 702 AAV79002 363 18 Staphylococcus aur  
c 703 AAI82131 363 22 Human polynucleoti  
c 704 ABV56939 364 23 Human prostate exp  
c 705 ABX91943 364 25 Human G protein-co  
c 706 AAS58961 365 22 Human cancer relat  
c 707 AAV78401 367 18 Staphylococcus aur  
c 708 AAL08266 370 22 Human breast cance  
709 ABK92401 370 24 Human prostate spe  
710 AAA98496 373 21 Vicuna PTEN/MMAC1  
c 711 AAL08328 374 22 Human breast cance  
712 AAL11395 374 22 Human breast cance  
c 713 AAI91055 374 22 Human polynucleoti  
714 AAN71112 375 8 sequence of PstI f  
715 AAV78357 375 18 Staphylococcus aur  
c 716 AAL53485 375 24 RNase P RNA region  
c 717 AAV78311 377 18 Staphylococcus aur  
c 718 ABV19383 377 23 Human prostate exp  
c 719 AAV76517 379 18 Staphylococcus aur  
c 720 ABV16745 379 23 Human prostate exp  
c 721 AAV78457 380 18 Staphylococcus aur  
722 AAV78387 380 18 Human prostate exp  
c 723 ABV18844 381 23 Staphylococcus aur  
724 AAV78304 383 18 Staphylococcus aur  
725 AAV78613 385 18 Human polynucleoti  
726 AAI81278 385 22 Staphylococcus aur  
727 AAV78373 386 18 Human polynucleoti  
c 728 AAV78373 386 18 Staphylococcus aur  
729 AAS43398 388 22 DNA encoding novel  
730 AAI83763 388 22 Human polynucleoti  
731 AAS83299 388 23 DNA encoding novel  
c 732 AAS58886 389 22 Human cancer relat  
c 733 AAS84418 389 23 DNA encoding novel  
734 ABZ71627 389 25 Breast specific nu  
735 AAS59156 391 22 Human cancer relat  
736 AAS91523 391 23 DNA encoding novel  
c 737 AAI83186 393 22 Human polynucleoti  
c 738 AAS81263 393 23 DNA encoding novel

394 AAV78194 18 Staphylococcus aur  
395 AAF14421 21 Aspergillus oryzae  
395 AAS59135 22 Human cancer relat  
395 ABV24133 23 Human prostate exp  
395 ABV29778 23 Human prostate exp  
396 AAS59148 22 Human cancer relat  
397 AAL09123 22 Human breast cance  
397 ABV18183 23 Human prostate exp  
397 AAS85438 23 DNA encoding novel  
398 AAQ51194 14 Plasmilar gene. U  
399 AAV77304 18 Staphylococcus aur  
399 AAV75654 18 Staphylococcus aur  
400 AAV78299 18 Staphylococcus aur  
400 AAV78283 18 Staphylococcus aur  
400 AAV78260 18 Staphylococcus aur  
400 AAV78212 18 Staphylococcus aur  
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400 AAV78174 18 Staphylococcus aur  
400 AAV78156 18 Staphylococcus aur  
400 AAV78165 18 Staphylococcus aur  
400 AAV78142 18 Staphylococcus aur  
400 AAV78133 18 Staphylococcus aur  
400 AAV78110 18 Staphylococcus aur  
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400 AAV78099 18 Staphylococcus aur  
400 AAV78085 18 Staphylococcus aur  
400 AAV78029 18 Staphylococcus aur  
400 AAV78000 18 Staphylococcus aur  
400 AAV78002 18 Staphylococcus aur  
400 AAV77980 18 Staphylococcus aur  
400 AAV77982 18 Staphylococcus aur  
400 AAV77954 18 Staphylococcus aur  
400 AAV77918 18 Staphylococcus aur  
400 AAV77893 18 Staphylococcus aur  
400 AAV77859 18 Staphylococcus aur  
400 AAV76748 18 Staphylococcus aur  
400 AAV76692 18 Staphylococcus aur  
400 AAV76420 18 Staphylococcus aur  
400 AAV76366 18 Staphylococcus aur  
400 AAV78545 18 Staphylococcus aur  
400 AAV78545 18 Staphylococcus aur  
400 AAV78514 18 Staphylococcus aur  
400 AAV78464 18 Staphylococcus aur  
400 AAV78427 18 Staphylococcus aur  
400 AAV78436 18 Staphylococcus aur  
400 AAV78394 18 Staphylococcus aur  
400 AAV78343 18 Staphylococcus aur  
400 AAV78350 18 Staphylococcus aur  
400 AAV78329 18 Staphylococcus aur  
400 AAS63174 23 DNA encoding novel  
400 AAS85302 23 DNA encoding novel  
400 AAS85302 23 DNA encoding novel  
403 AAS59130 22 Human cancer relat  
403 ACAS7262 22 Human adipocyte Se  
404 AAS59108 22 Human cancer relat  
404 AAS59145 22 Human cancer relat  
404 ABK93122 24 Human prostate spe  
405 AAI80665 22 Human polynucleoti  
405 AAI81628 22 Human polynucleoti  
407 AAS59889 22 Human novel cytoki  
407 AAL11209 22 Human breast cance  
407 AAS84914 23 DNA encoding novel  
408 AAS733120 23 DNA encoding novel  
411 AAI89090 22 Human polynucleoti  
412 AAI83776 22 Human polynucleoti  
412 AAS66497 23 DNA encoding novel  
414 AAS67104 23 DNA encoding novel  
415 AAL08319 22 Human breast cance  
415 AAL08591 22 Human breast cance  
415 AAI85235 22 Human polynucleoti  
415 ACAS7236 25 Human adipocyte Se



812	27	10.8	416	23	AAS86840	DNA encoding novel	c 885	27	10.8	464	23	ABV17986	Human prostate exp
813	27	10.8	416	23	AAS87940	DNA encoding novel	c 886	27	10.8	464	23	AAS68866	DNA encoding novel
814	27	10.8	417	22	AAI84628	Human polynucleoti	887	27	10.8	465	6	AAN50760	Sequence of the hu
815	27	10.8	417	23	AAS67232	DNA encoding novel	888	27	10.8	467	25	ABZ71678	Breast specific nu
c 816	27	10.8	419	23	AAS76367	DNA encoding novel	889	27	10.8	468	23	AAS69012	DNA encoding novel
c 817	27	10.8	419	23	AAS82743	DNA encoding novel	c 890	27	10.8	468	23	AAS69012	DNA encoding novel
818	27	10.8	419	23	AAS82766	DNA encoding novel	891	27	10.8	468	23	AAS79790	DNA encoding novel
c 819	27	10.8	419	23	AAS83980	DNA encoding novel	c 892	27	10.8	468	23	AAS79790	DNA encoding novel
820	27	10.8	419	23	AAS85103	DNA encoding novel	893	27	10.8	470	22	AAI08280	Human breast cance
c 821	27	10.8	419	23	AAS88114	DNA encoding novel	c 894	27	10.8	470	22	AAI92703	Human polynucleoti
822	27	10.8	419	23	AAS89461	DNA encoding novel	895	27	10.8	471	22	AAI80595	Human polynucleoti
823	27	10.8	419	23	AAS89585	DNA encoding novel	c 896	27	10.8	476	23	AAS65767	DNA encoding novel
824	27	10.8	421	18	AAV75558	Staphylococcus aur	897	27	10.8	480	18	AAV78045	Staphylococcus aur
c 825	27	10.8	421	22	AAI09104	Human breast cance	c 898	27	10.8	483	23	AAS69581	DNA encoding novel
c 826	27	10.8	421	23	AAS68848	DNA encoding novel	c 899	27	10.8	486	23	AAS65480	DNA encoding novel
827	27	10.8	422	22	AAI67309	Novel human polynu	900	27	10.8	487	24	AAI39983	Lung-specific nucl
c 828	27	10.8	423	22	AAI64895	Xanthomonas hrfl p	c 901	27	10.8	488	22	AAI88888	Human polynucleoti
c 829	27	10.8	424	23	AAS65993	DNA encoding novel	c 902	27	10.8	490	22	AAI88885	Human polynucleoti
c 830	27	10.8	424	23	AAS72383	DNA encoding novel	c 903	27	10.8	490	23	ABV18701	Human prostate exp
831	27	10.8	424	23	AAS87647	DNA encoding novel	904	27	10.8	490	23	AAS87979	DNA encoding novel
c 832	27	10.8	426	23	AAS68333	DNA encoding novel	905	27	10.8	493	22	AAI68095	Human lung tumour
833	27	10.8	427	24	ABA91372	Human breast speci	906	27	10.8	493	24	ABK38006	cDNA encoding clon
c 834	27	10.8	428	22	AAI08981	Human breast cance	907	27	10.8	493	25	ACA10335	Human lung cancer-
c 835	27	10.8	429	22	AAS59154	Human cancer relat	908	27	10.8	493	25	ABX99286	Lung cancer therap
836	27	10.8	429	22	AAI84007	Human polynucleoti	c 909	27	10.8	494	18	AAV78322	Staphylococcus aur
c 837	27	10.8	430	22	AAI10892	Human breast cance	c 910	27	10.8	495	22	AAI87721	Human polynucleoti
838	27	10.8	433	22	AAI08819	Human breast cance	911	27	10.8	496	24	ABQ73822	Human colon specif
839	27	10.8	434	23	AAS70099	DNA encoding novel	912	27	10.8	498	23	AAS72533	DNA encoding novel
c 840	27	10.8	434	24	ABL98893	Omega-conopeptide	913	27	10.8	498	23	AAS72567	DNA encoding novel
841	27	10.8	435	23	AAS89454	DNA encoding novel	c 914	27	10.8	498	23	AAS81004	DNA encoding novel
c 842	27	10.8	436	18	AAV75752	Staphylococcus aur	915	27	10.8	501	18	AAV74965	Staphylococcus aur
c 843	27	10.8	436	23	AAS64836	DNA encoding novel	c 916	27	10.8	503	24	ABK53643	Human eosinophil-m
844	27	10.8	436	23	AAS79231	DNA encoding novel	c 917	27	10.8	511	22	AAI93225	cDNA encoding SRT
845	27	10.8	436	23	AAS83912	DNA encoding novel	918	27	10.8	511	24	ABK53647	Human eosinophil-m
c 846	27	10.8	436	23	AAS84547	DNA encoding novel	c 919	27	10.8	512	23	ABV16864	Human prostate exp
847	27	10.8	436	23	AAS85105	DNA encoding novel	c 920	27	10.8	514	18	AAV75344	Staphylococcus aur
848	27	10.8	437	22	AAI81478	Human polynucleoti	c 921	27	10.8	514	23	ABV18541	Human prostate exp
c 849	27	10.8	437	23	ABV58188	Human prostate exp	922	27	10.8	516	21	AAA98502	Quail PTEN/MMAC1
c 850	27	10.8	438	23	AAS73611	DNA encoding novel	c 923	27	10.8	516	23	ABV25904	Human prostate exp
c 851	27	10.8	438	23	AAS75599	DNA encoding novel	c 924	27	10.8	516	23	ABV25905	Human prostate exp
c 852	27	10.8	438	23	AAS76838	DNA encoding novel	c 925	27	10.8	516	23	ABV29948	Human prostate exp
c 853	27	10.8	438	23	AAS83175	DNA encoding novel	c 926	27	10.8	517	23	ABV24067	Human prostate exp
c 854	27	10.8	438	25	ABZ18200	Group III cDNA can	927	27	10.8	519	22	AAI86819	Human polynucleoti
c 855	27	10.8	440	24	ABQ59714	Human colon cancer	928	27	10.8	520	22	AAI93082	Human polynucleoti
856	27	10.8	441	23	AAS83978	DNA encoding novel	c 929	27	10.8	524	23	ABV16560	Human prostate exp
857	27	10.8	441	23	AAS88169	DNA encoding novel	c 930	27	10.8	524	23	ABV19795	Human prostate exp
858	27	10.8	441	23	AAS89460	DNA encoding novel	931	27	10.8	524	23	ABV55409	Human prostate exp
c 859	27	10.8	442	23	AAS75343	DNA encoding novel	c 932	27	10.8	527	24	ABQ92829	Triticum tauschii/
c 860	27	10.8	442	23	AAS87088	DNA encoding novel	c 933	27	10.8	531	23	ABV19061	Human prostate exp
c 861	27	10.8	444	23	AAS91551	DNA encoding novel	934	27	10.8	531	23	ABV21169	Human prostate exp
c 862	27	10.8	445	22	AAI08420	Human breast cance	935	27	10.8	531	23	ABV26983	Human prostate exp
c 863	27	10.8	445	22	AAI08583	Human breast cance	936	27	10.8	532	22	ABA09461	Human adapter prot
c 864	27	10.8	447	23	ABV19306	Human prostate exp	c 937	27	10.8	535	18	AAV75339	Staphylococcus aur
c 865	27	10.8	447	25	ACA57254	Human adipocyte Se	c 938	27	10.8	535	24	ABK53467	Human eosinophil-m
c 866	27	10.8	448	23	ABV18787	Human prostate exp	939	27	10.8	542	23	AAS82990	DNA encoding novel
c 867	27	10.8	448	23	ABV18927	Human prostate exp	c 940	27	10.8	542	23	AAS82990	DNA encoding novel
868	27	10.8	448	23	AAS80440	DNA encoding novel	941	27	10.8	544	24	ABK97867	Rat ARP-2 cDNA var
869	27	10.8	448	23	AAS88157	DNA encoding novel	c 942	27	10.8	551	18	AAV75767	Staphylococcus aur
c 870	27	10.8	451	18	AAV75120	Staphylococcus aur	c 943	27	10.8	551	23	AAS84015	DNA encoding novel
c 871	27	10.8	451	18	AAV74934	Staphylococcus aur	c 944	27	10.8	552	24	ABK92454	Human prostate spe
872	27	10.8	451	22	AAI87457	Human polynucleoti	c 945	27	10.8	554	23	ABV19318	Human prostate exp
873	27	10.8	451	23	AAS84020	DNA encoding novel	c 946	27	10.8	555	23	ABV30269	Human prostate exp
c 874	27	10.8	452	23	AAS78257	DNA encoding novel	947	27	10.8	558	18	AAV74434	Staphylococcus aur
c 875	27	10.8	453	23	ABV17869	Human prostate exp	c 948	27	10.8	560	18	AAV78596	Staphylococcus aur
c 876	27	10.8	454	19	AAV18860	cDNA for tarantula	c 949	27	10.8	562	23	ABV22543	Human prostate exp
877	27	10.8	454	23	AAS66075	DNA encoding novel	c 950	27	10.8	562	23	ABV22547	Human prostate exp
c 878	27	10.8	455	22	AAI08178	Human breast cance	c 951	27	10.8	562	23	ABV27155	Human prostate exp
879	27	10.8	455	23	AAS84918	DNA encoding novel	c 952	27	10.8	562	23	ABV28358	Human prostate exp
c 880	27	10.8	459	23	AAS82876	DNA encoding novel	c 953	27	10.8	562	23	ABV28362	Human prostate exp
881	27	10.8	460	18	AAV74987	Staphylococcus aur	c 954	27	10.8	563	23	ABV20012	Human prostate exp
882	27	10.8	460	23	AAS76947	DNA encoding novel	c 955	27	10.8	563	23	ABV21336	Human prostate exp
c 883	27	10.8	463	22	AAI08929	Human breast cance	c 956	27	10.8	565	23	AAS68334	DNA encoding novel
c 884	27	10.8	463	23	ABV18369	Human prostate exp	c 957	27	10.8	568	23	ABV18869	Human prostate exp

C 958 27 10.8 571 18 AAV75287  
959 27 10.8 572 24 ABT03348  
960 27 10.8 573 18 AAV74318  
961 27 10.8 574 21 AAF12679  
C 962 27 10.8 581 23 ABV19123  
C 963 27 10.8 583 21 AAF12575  
C 964 27 10.8 586 23 ABV53788  
965 27 10.8 587 18 AAV75181  
C 966 27 10.8 587 18 AAV75181  
C 967 27 10.8 588 23 AAS68054  
C 968 27 10.8 589 23 AAS81476  
C 969 27 10.8 597 22 AAI92945  
C 970 27 10.8 600 18 AAV75587  
C 971 27 10.8 600 24 ABK81409  
972 27 10.8 600 24 ABK47942  
C 973 27 10.8 600 24 ABK47942  
974 27 10.8 605 21 AAF14197  
C 975 27 10.8 607 24 ABK93126  
C 976 27 10.8 609 21 AA253510  
C 977 27 10.8 612 25 AB218345  
C 978 27 10.8 615 18 AAV75248  
C 979 27 10.8 619 23 ABV19101  
980 27 10.8 622 20 AAX32269  
981 27 10.8 622 21 AAF12782  
982 27 10.8 622 21 AAA09804  
983 27 10.8 622 23 ABV18446  
C 984 27 10.8 622 23 ABV18446  
C 985 27 10.8 627 23 ABV18909  
C 986 27 10.8 628 23 ABV16374  
C 987 27 10.8 628 25 AB218412  
C 988 27 10.8 629 12 AAQ11117  
C 989 27 10.8 631 18 AAV75003  
C 990 27 10.8 635 23 AAS67324  
991 27 10.8 636 18 AAV77975  
992 27 10.8 638 18 AAV75395  
993 27 10.8 640 13 AAQ29866  
C 994 27 10.8 642 23 ABV60693  
C 995 27 10.8 643 23 AAS67419  
C 996 27 10.8 645 23 ABV19141  
C 997 27 10.8 645 23 ABV60357  
C 998 27 10.8 646 23 ABV18665  
C 999 27 10.8 647 22 AAH73232  
C1000 27 10.8 647 23 AAS77650

ALIGNMENTS

RESULT 1  
AAF22280  
ID AAF22280 standard; DNA; 67087 BP.  
XX  
AC AAF22280;  
XX  
DT 20-MAR-2001 (first entry)  
XX  
DE BAC containing repeats from centromeres 1-4 #3.  
XX  
KW Centromere; michrosome; vector; ds.  
XX  
OS Arabidopsis thaliana.  
XX  
PN WO200055325-A2.  
XX  
PD 21-SEP-2000.  
XX  
PF 17-MAR-2000; 2000WO-US07392.  
XX  
PR 18-MAR-1999; 99US-0125219.  
PR 01-APR-1999; 99US-0127409.  
PR 18-MAY-1999; 99US-0134770.  
PR 13-SEP-1999; 99US-0153584.  
PR 17-SEP-1999; 99US-0154603.

Staphylococcus aur  
Ovary cell-specifi  
Staphylococcus aur  
Aspergillus oryzae  
Human prostate exp  
Aspergillus oryzae  
Human prostate exp  
Staphylococcus aur  
Staphylococcus aur  
DNA encoding novel  
DNA encoding novel  
Human polynucleoti  
Staphylococcus aur  
Modified DNA encod  
Human Jun B Proto-  
Human Jun B Proto-  
Aspergillus oryzae  
Human prostate spe  
Neisseria meningit  
Group III cDNA can  
Staphylococcus aur  
Human prostate exp  
Nucleotide sequenc  
Aspergillus oryzae  
Human nuclear rece  
Human prostate exp  
Human prostate exp  
Human prostate exp  
Group III cDNA can  
Exon 1 of Human lu  
Staphylococcus aur  
DNA encoding novel  
Staphylococcus aur  
Staphylococcus aur  
Pheromone receptor  
Human prostate exp  
DNA encoding novel  
Human prostate exp  
Human prostate exp  
Human prostate exp  
Human cervical can  
DNA encoding novel

XX (UYCH-) UNIV CHICAGO.  
PA  
XX  
PI Preuss D, Copenhaver G, Keith K;  
XX  
DR WPI; 2000-587529/55.  
XX  
PT Recombinant DNA construct comprising a plant centromere, useful for  
PT producing stably inherited michrosomes which can serve as vectors for  
PT the construction of transgenic plant and animal cells -  
XX  
PS Claim 102; Page 336-351; 1449pp; English.  
XX  
CC The present invention relates to a recombinant DNA construct of a plant  
CC (Arabidopsis thaliana) centromere. The constructs are useful for  
CC producing stably inherited michrosomes which can serve as vectors for  
CC the construction of transgenic plant and animal cells expressing  
CC selected proteins such as hormones, enzymes, interleukins, clotting  
CC factors, cytokines, antibodies, and growth factors.  
XX  
SQ Sequence 67087 BP; 20469 A; 12665 C; 12858 G; 20613 T; 482 other;  
  
Query Match 12.7%; Score 32; DB 21; Length 67087;  
Best Local Similarity 100.0%; Pred. No. 5.3e-06;  
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 93 AAAAATCNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 124  
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
Db 38392 AAAAATCNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 38423  
  
RESULT 2  
ACA57265/c  
ID ACA57265 standard; cDNA; 409 BP.  
XX  
AC ACA57265;  
XX  
DT 10-JUN-2003 (first entry)  
XX  
DE Human adipocyte Selected Interacting domain, SID, cDNA #352.  
XX  
KW Human; ss; gene; prey; adipocyte; SID; selected interacting domain;  
KW anorectic; antidiabetic; protein-protein interaction; diabetes;  
KW yeast 2-hybrid assay; metabolic disorder; obesity.  
XX  
OS Homo sapiens.  
XX  
FN WO200286122-A2.  
XX  
PD 31-OCT-2002.  
XX  
PF 14-MAR-2002; 2002WO-EP03768.  
XX  
PR 14-MAR-2001; 2001US-275734P.  
XX  
PA (HYBR-) HYBRIGENICS.  
XX  
PI Legrain P, Daviet L;  
XX  
DR WPI; 2003-103412/09.  
DR P-PSDB; ABU70721.  
XX  
PT New complex between two interacting proteins in adipocyte cells, useful  
PT for identifying selected interacting domains that modulate protein  
PT interactions, or for preventing or treating metabolic disorders such as  
PT obesity or diabetes -  
XX  
PS Claim 7; Page 223-224; 382pp; English.  
XX  
CC The invention relates to a complex between two interacting proteins in  
CC adipocyte cells, given in the specification. The proteins are identified  
CC by selecting a bait protein from a known adipocyte marker and then  
CC performing a yeast 2-hybrid selection to isolate prey proteins encoded by

CC members of an adipocyte cDNA library. The proteins are designated SID  
CC (RTM) (selected interacting domains) proteins. Also included are a  
CC polynucleotide encoding a polypeptide in the adipocyte cells, a  
CC recombinant host cell expressing at least one of the interacting  
CC polypeptides of the complex, selecting a modulating compound in adipocyte  
CC cells, a SID (RTM) polypeptide comprising any of the 738 amino acid  
CC sequences given in the specification (including its fragment or variant),  
CC a SID (RTM) polynucleotide comprising any of the 738 nucleotide sequences  
CC given in the specification (including its fragment or variant), a vector  
CC comprising the SID (RTM) polynucleotide, a recombinant host cell  
CC comprising the vector, a protein chip comprising the polypeptides and  
CC a record comprising all or part of the data, listed in the specification.  
CC The complex, polypeptides, polynucleotides and compounds are  
CC useful for preventing or treating metabolic disorders such as obesity  
CC or diabetes. The polynucleotides are useful as probes or primers. The  
CC complex is particularly useful for identifying selected interacting  
CC domains (SID (RTM)) for screening drugs that modulate the protein  
CC interaction, thus exhibiting the therapeutic effect. The present  
CC sequence encodes a SID (prey) protein of the invention.  
XX  
SQ Sequence 409 BP; 71 A; 68 C; 69 G; 105 T; 96 other;

Query Match 12.4%; Score 31; DB 25; Length 409;  
Best Local Similarity 100.0%; Pred. No. 2.2e-05;  
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 94 AAAATCNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 124  
DB 89 AAAATCNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 59  
|||||

RESULT 3  
ABZ20367/c  
ID ABZ20367 standard; cDNA; 765 BP.  
XX  
AC ABZ20367;  
XX  
DT 23-JAN-2003 (first entry)  
XX  
DE Oncofoetal cDNA sequence overexpressed in tumour tissue SEQ ID NO:2794.  
XX  
QW Human; cancer; tumour; therapy; diagnosis; CT antigen; CP antigen;  
QW immune response; virology; immunology; microbiology; molecular biology;  
QW recombinant DNA technology; gene; ss.  
XX  
XS Homo sapiens.  
XX  
YN WO200278516-A2.  
XD  
XD 10-OCT-2002.  
XX  
XF 28-MAR-2002; 2002WO-US10421.  
XX  
XP 30-MAR-2001; 2001US-280255P.  
XP 28-AUG-2001; 2001US-315563P.  
XP 09-JAN-2002; 2002US-347313P.  
XX  
PA (CORI-) CORIXA CORP.  
XX  
PI Wang T, Wang S, Bangur CS, Gaiger A;  
XX  
PI WPI; 2003-058387/05.  
XX  
DR New immunogenic polynucleotides or polypeptides useful for diagnosing,  
XX preventing and treating cancer expressing CT or CP mRNA antigens, and  
XX in virology, immunology, microbiology, molecular biology and  
XX recombinant DNA techniques -  
XX  
XS Claim 1; SEQ ID 2794; 207pp; English.  
XX  
XS ABQ17575 to ABQ20506 represent isolated polynucleotide (I) sequences, and  
XX ABP54446 to ABP54472 represent protein (II) sequences, from the present  
XX invention. (I) and (II) have cytostatic activity and can be used in gene

CC therapy and vaccines. (I), (II), antibodies and compositions from the  
CC present invention are useful for diagnosing, preventing and treating  
CC cancer, which expresses CT or CP mRNA antigens. They are useful for  
CC stimulating immune response. They can also be useful in virology,  
CC immunology, microbiology, molecular biology and recombinant DNA  
CC techniques.  
CC N.B. The sequence data for this patent did not form part of the printed  
CC specification, but was obtained in electronic format directly from WIPO  
CC at ftp.wipo.int/pub/published\_pct\_sequences.  
XX  
SQ Sequence 765 BP; 211 A; 123 C; 106 G; 266 T; 59 other;  
  
Query Match 12.4%; Score 31; DB 25; Length 765;  
Best Local Similarity 100.0%; Pred. No. 2.1e-05;  
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 94 AAAATCNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 124  
DB 282 AAAATCNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 252  
|||||

RESULT 4  
AAV99321/c  
ID AAV99321 standard; cDNA; 1075 BP.  
XX  
AC AAV99321;  
XX  
DT 25-MAR-1999 (first entry)  
XX  
DE GDNFR-alpha cDNA clone 2.  
XX  
KW Human; glial cell-line derived neurotrophic factor receptor-alpha;  
KW GDNFR-alpha; glial cell line-derived neurotrophic factor; GDNF;  
KW neurturin; signal transduction; dopaminergic nerve cell;  
KW Parkinson's disease; Alzheimer's disease; amyotrophic lateral sclerosis;  
KW neurological disorder; diabetes; glaucoma; sensory neuron;  
KW retinal ganglion cell degeneration; sensory neuropathy;  
KW retinopathy; gene therapy; ss.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT CDS 2..445  
FT /\*tag= a  
XX  
PN WO9854213-A2.  
XX  
PD 03-DEC-1998.  
XX  
PF 27-APR-1998; 98WO-US08486.  
XX  
PR 30-MAY-1997; 97US-0866354.  
XX  
PA (AMGE-) AMGEN INC.  
XX  
PI Fox GM, Jing S, Wen D;  
XX  
DR WPI; 1999-080806/07.  
DR p-PSDB; AAW84172.  
XX  
XX New isolated glial cell line-derived neurotrophic factor receptors -  
XX used to develop products for treating e.g. improperly functioning  
XX dopaminergic nerve cells, Parkinson's disease, Alzheimer's disease  
XX or amyotrophic lateral sclerosis  
XX  
XS Example 6; Page 148-149; 318pp; English.  
XX  
XS The present sequence represents a cDNA clone insert encoding a  
XX human glial cell-line derived neurotrophic factor receptor-alpha  
XX (GDNFR-alpha). The protein is capable of complexing with glial  
XX cell line-derived neurotrophic factor (GDNF) and mediating cell  
XX response to GDNF. GDNFR-alpha proteins are functionally characterised  
XX by the ability to bind GDNF and/or neurturin specifically, and to act

CC as part of a molecular complex which mediates or enhances the signal  
CC transduction affects of GDNF and/or neurturin. The proteins can be used  
CC for treating improperly functioning dopaminergic nerve cells,  
CC Parkinson's disease, Alzheimer's disease or amyotrophic lateral  
CC sclerosis. They can also be used for treating neurological disorders  
CC associated with diabetes, glaucoma or other diseases and conditions  
CC involving retinal ganglion cell degeneration, sensory neuropathy caused  
CC by injury to, insults to, or degeneration of, sensory neurons,  
CC pathological conditions, or disease or injury-related retinopathies.  
CC The products can also be used for detection, diagnosis, drug screening  
CC and gene therapy.  
XX  
SQ Sequence 1075 BP; 296 A; 225 C; 205 G; 310 T; 39 other;  
  
Query Match 12.4%; Score 31; DB 20; Length 1075;  
Best Local Similarity 100.0%; Pred. No. 2e-05;  
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 94 AAAATCTNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 124  
|||||  
Db 807 AAAATCTNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 777  
  
RESULT 5  
ABK10773  
ID ABK10773 standard; DNA; 1200 BP.  
XX  
AC ABK10773;  
XX  
DT 18-JUN-2002 (first entry)  
XX  
DE Human SCYA26 modified DNA.  
XX  
KW Human; small inducible cytokine subfamily A (Cys-Cys) member 26; SCYA26;  
KW respiratory inflammatory disease; single nucleotide polymorphism; ds;  
KW haplotyping; haplotype pair; gene therapy; antiinflammatory; respiratory;  
KW gene.  
XX  
OS Homo sapiens.  
OS Synthetic.  
XX  
PN WO200216400-A2.  
XX  
PD 28-FEB-2002.  
XX  
PF 27-AUG-2001; 2001WO-US26664.  
XX  
PR 25-AUG-2000; 2000US-227965P.  
XX  
PA (GENA-) GENAISSANCE PHARM INC.  
XX  
PI Bieglecki KM, Han J, Kliem SE, Sausker EA;  
XX  
DR WPI; 2002-280908/32.  
XX  
PT Novel isolated polynucleotide which is a polymorphic variant of small  
PT inducible cytokine subfamily A (Cys-Cys), member 26 (SCYA26) gene  
PT useful for expressing SCYA26 protein isoform used in drug screening  
PT techniques -  
XX  
PS Example 2; Page 78-79; 79pp; English.  
XX  
CC The invention relates to single nucleotide polymorphisms in the gene  
CC encoding human small inducible cytokine subfamily A (Cys-Cys) member 26  
CC (SCYA26). A method for haplotyping the SCYA26 gene in an individual  
CC comprises identifying the nucleotide at one or more polymorphic sites and  
CC determining whether one of the copies of the gene is defined by one of  
CC the SCYA26 haplotypes given in the specification or whether both copies  
CC are defined by a haplotype pair. This method is useful in genotyping,  
CC whereby all possible haplotype pairs can be assigned to specific  
CC genotypes. An association between a trait and a haplotype or haplotype  
CC pair of the SCYA26 gene can be identified by comparing the frequency of  
CC the haplotype or haplotype pair in a population exhibiting the trait with

CC the frequency of the haplotype or haplotype pair in a reference  
CC population, where a higher haplotype frequency in the trait population  
CC indicates the trait is associated with the haplotype or haplotype pair.  
CC SCYA26 and its corresponding DNA are used for studying the expression and  
CC function of SCYA26, for use in screening for candidate drugs to treat  
CC diseases related to SCYA26 activity, such as respiratory inflammatory  
CC diseases. The sequences are also useful for studying the effect of  
CC variation on the biological activity of SCYA26 as well as on the binding  
CC affinity of candidate drugs targeting SCYA26. This sequence represents  
CC a human SCYA26 modified DNA used in electronic searching of SCYA26  
CC haplotypes.  
XX  
SQ Sequence 1200 BP; 114 A; 189 C; 148 G; 139 T; 610 other;  
  
Query Match 12.4%; Score 31; DB 24; Length 1200;  
Best Local Similarity 100.0%; Pred. No. 2e-05;  
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 100 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNTTCCAA 130  
|||||  
Db 696 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNTTCCAA 726  
  
RESULT 6  
AAD43682  
ID AAD43682 standard; DNA; 1560 BP.  
XX  
AC AAD43682;  
XX  
DT 14-NOV-2002 (first entry)  
XX  
DE Human interleukin 15 (IL15) gene fragment allelic variant DNA.  
XX  
KW Human; interleukin 15; IL15; haplotype; polymorphic site; PS;  
KW drug screening; infection; human immunodeficiency virus; leukaemia;  
KW transgenic animal; anti-inflammatory; cytostatic; antibacterial;  
KW gene therapy; ds.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT misc\_feature 30  
FT /\*tag= a  
FT /note= "Polymorphic site, PS1"  
FT 150  
FT /\*tag= b  
FT /note= "Polymorphic site, PS2"  
FT 270  
FT /\*tag= c  
FT /note= "Polymorphic site, PS3"  
FT 390  
FT /\*tag= d  
FT /note= "Polymorphic site, PS4"  
FT 510  
FT /\*tag= e  
FT /note= "Polymorphic site, PS5"  
FT 630  
FT /\*tag= f  
FT /note= "Polymorphic site, PS6"  
FT 750  
FT /\*tag= g  
FT /note= "Polymorphic site, PS7"  
FT 870  
FT /\*tag= h  
FT /note= "Polymorphic site, PS8"  
FT 990  
FT /\*tag= i  
FT /note= "Polymorphic site, PS9"  
FT 1110  
FT /\*tag= j  
FT /note= "Polymorphic site, PS10"  
FT 1230  
FT /\*tag= k







D AAV99312 standard; cDNA; 3209 BP.  
XX AAV99312;  
XX 25-MAR-1999 (first entry)  
XX Glial cell-line derived neurotrophic factor receptor-alpha cDNA clone.  
DE Human; glial cell-line derived neurotrophic factor receptor-alpha;  
XX GDNFR-alpha; glial cell line-derived neurotrophic factor; GDNF;  
KW neurturin; signal transduction; dopaminergic nerve cell;  
KW Parkinson's disease; Alzheimer's disease; amyotrophic lateral sclerosis;  
KW neurological disorder; diabetes; glaucoma; sensory neuron;  
KW retinal ganglion cell degeneration; sensory neuropathy;  
KW retinopathy; gene therapy; ss.  
XX Homo sapiens.  
OS  
XX  
XX Key Location/Qualifiers  
FH 540..1937  
FT CDS /\*tag= a  
FT  
FT  
FT  
XX WO9854213-A2.  
XX 03-DEC-1998.  
XX  
XX 27-APR-1998; 98WO-US08486.  
XX  
XX 30-MAY-1997; 97US-0866354.  
XX (AMGE-) AMGEN INC.  
XX  
XX Fox GM, Jing S, Wen D;  
PPI WPI; 1999-080806/07.  
XX P-PSDB; AAW84165.  
XX  
XX New isolated glial cell line-derived neurotrophic factor receptors -  
PT used to develop products for treating e.g. improperly functioning  
PT dopaminergic nerve cells, Parkinson's disease, Alzheimer's disease  
PT or amyotrophic lateral sclerosis  
XX  
XX Example 6; Page 124-127; 318pp; English.  
XX  
XX The present sequence represents a cDNA clone insert encoding a  
CC human glial cell-line derived neurotrophic factor receptor-alpha  
CC (GDNFR-alpha). The protein is capable of complexing with glial  
CC cell line-derived neurotrophic factor (GDNF) and mediating cell  
CC response to GDNF. GDNFR-alpha proteins are functionally characterised  
CC by the ability to bind GDNF and/or neurturin specifically, and to act  
CC as part of a molecular complex which mediates or enhances the signal  
CC transduction affects of GDNF and/or neurturin. The proteins can be used  
CC for treating improperly functioning dopaminergic nerve cells,  
CC Parkinson's disease, Alzheimer's disease or amyotrophic lateral  
CC sclerosis. They can also be used for treating neurological disorders  
CC associated with diabetes, glaucoma or other diseases and conditions  
CC involving retinal ganglion cell degeneration, sensory neuropathy caused  
CC by injury to, insults to, or degeneration of, sensory neurons,  
CC pathological conditions, or disease or injury-related retinopathies.  
CC The products can also be used for detection, diagnosis, drug screening  
CC and gene therapy.  
XX  
XX Sequence 3209 BP; 822 A; 795 C; 756 G; 795 T; 41 other;

Query Match 12.4%; Score 31; DB 20; Length 3209;  
Best Local Similarity 100.0%; Pred. No. 1.9e-05;  
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94 AAAATCNNNNNNNNNNNNNNNNNNNNNNNNNNNN 124  
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RESULT 11  
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ID AAV74334 standard; DNA; 17310 BP.  
XX  
XX AC AAV74334;  
XX  
XX DT 16-MAR-1999 (first entry)  
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XX Staphylococcus aureus contig SEQ ID #23.  
KW Computer readable medium; vaccine; S.aureus infection; immunodetection;  
KW cellulitis; eyelid infection; food poisoning; osteomyelitis; therapy;  
KW skin infection; surgical wound infection; scalded skin syndrome;  
KW toxic shock syndrome; ds.  
XX  
XX Staphylococcus aureus.  
OS  
XX  
XX Key Location/Qualifiers  
FH 721..780  
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FT are included to maintain the nucleotide numbering  
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FT /note= "these bases represent a line of missing text in  
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FT are included to maintain the nucleotide numbering  
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given in the specification for this DNA sequence"
EP786519-A2.
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XX
XX
30-JUL-1997.
PD
XX
XX
07-JAN-1997; 97EP-0100117.
PF
XX
XX
05-JAN-1996; 96US-0009861.
PR
XX
XX
(HUMA-) HUMAN GENOME SCI INC.
PA
XX
XX
Barash SC, Choi GH, Dillon PJ, Fannon MR, Kunsch CA;
PI
PI
XX
XX
WPI; 1997-374922/35.
DR
XX
XX
Polynucleotide(s) and proteins derived from Staphylococcus aureus -
stored on computer readable medium and used in the production of
anti-S.aureus vaccines
PT
PT
XX
XX
Claim 1; Page 283-293; 3271pp; English.
PS
XX
XX
This sequence represents one of 5191 Staphylococcus aureus DNA sequences
of the invention. The DNA sequences are recorded on a computer readable
medium, preferably selected from a floppy or hard disk, random access
memory (RAM), read-only memory (ROM) or CD-ROM. Homology searches using
the S.aureus DNA sequences allows putative functions to be assigned so
that protein-encoding or regulatory regions of commercial, therapeutic or
industrial importance can be obtained. Specifically, sequences which are
likely to encode antigens have been identified and these polypeptides can
be used in a vaccine composition against S.aureus infection. The
polypeptides can also be used in a kit for the immunodetection of
S.aureus in a sample. S.aureus is implicated in numerous human diseases,
including cellulitis, eyelid infections, food poisoning, osteomyelitis,
skin and surgical wound infections, scalded skin syndrome, toxic shock
syndrome, etc. Organisms transformed with the DNA sequences can be used
for recombinant production of the polypeptides. The new DNA sequences
(and their fragments) are useful as primers or probes for isolating
homologues of any of the S.aureus DNA sequences contained on the
computer readable medium.
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3Q Sequence 17310 BP; 5125 A; 3350 C; 2549 G; 5683 T; 603 other;

Query Match 12.4%; Score 31; DB 18; Length 17310;
Best Local Similarity 100.0%; Pred. No. 1.7e-05;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0

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RESULT 12
AAS93468
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AC AAS93468;
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DT 13-FEB-2002 (first entry)
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DE DNA encoding novel human diagnostic protein #29272.
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KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW food supplement; medical imaging; diagnostic; genetic disorder; ss.
XX
DS Homo sapiens.
XX
PN WO200175067-A2.

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XX	11-OCT-2001.
PD	
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XX	30-MAR-2001; 2001WO-US08631.
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XX	31-MAR-2000; 2000US-0540217.
PR	
PR	23-AUG-2000; 2000US-0649167.
XX	
XX	(HYSE-) HYSEQ INC.
PA	
XX	
PI	Drmanac RT, Liu C, Tang YT;
XX	
XX	WPI; 2001-639362/73.
DR	P-PSDB; ABG29281.
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XX	New isolated polynucleotide and encoded polypeptides, useful in
PT	diagnostics, forensics, gene mapping, identification of mutations
PT	responsible for genetic disorders or other traits and to assess
PT	biodiversity .
XX	
XX	Claim 1; SEQ ID No 29272; i03pp; English.
PS	
XX	
CC	The invention relates to isolated polynucleotide (I) and
CC	polypeptide (II) sequences. (I) is useful as hybridisation probes,
CC	polymerase chain reaction (PCR) primers, oligomers, and for chromosome
CC	and gene mapping, and in recombinant production of (II). The
CC	polynucleotides are also used in diagnostic production as expressed sequence tags
CC	for identifying expressed genes. (I) is useful in gene therapy techniques
CC	to restore normal activity of (II) or to treat disease states involving
CC	(II). (II) is useful for generating antibodies against it, detecting or
CC	quantitating a polypeptide in tissue, as molecular weight markers and as
CC	a food supplement. (II) and its binding partners are useful in medical
CC	imaging of sites expressing (II). (I) and (II) are useful for treating
CC	disorders involving aberrant protein expression or biological activity.
CC	The polypeptide and polynucleotide sequences have applications in
CC	diagnostics, forensics, gene mapping, identification of mutations
CC	responsible for genetic disorders or other traits to assess biodiversity
CC	and to produce other types of data and products dependent on DNA and
CC	amino acid sequences. AAS64197-AAS94564 represent novel human
CC	diagnostic coding sequences of the invention.
CC	Note: The sequence data for this patent did not appear in the printed
CC	specification, but was obtained in electronic format directly from WIPO
CC	at ftp.wipo.int/pub/published_pct_sequences.
XX	
SQ	Sequence 369 BP; 79 A; 88 C; 88 G; 85 T; 29 other;
	Query Match 12.0%; Score 30; DB 23; Length 369;
	Best Local Similarity 100.0%; Pred. No. 6.7e-05;
	Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0
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	RESULT 13
	AAV77943
ID	AAV77943 standard; DNA; 400 BP.
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AC	AAV77943;
XX	
DT	16-MAR-1999 (first entry)
XX	
DE	Staphylococcus aureus contig SEQ ID #3632.
XX	
KW	Computer readable medium; vaccine; S.aureus infection; immunodetection;
KW	cellulitis; eyelid infection; food poisoning; osteomyelitis; therapy;
KW	skin infection; surgical wound infection; scalded skin syndrome;
KW	toxic shock syndrome; ds.
XX	
OS	Staphylococcus aureus.
XX	
FH	Key Location/Qualifiers





KW skin infection; surgical wound infection; scalded skin syndrome;  
KW toxic shock syndrome; ds.  
XX  
XX  
OS Staphylococcus aureus.  
XX  
PH Key Location/Qualifiers  
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FT are included to maintain the nucleotide numbering  
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XX  
PN EP786519-A2.  
XX  
XX  
PD 30-JUL-1997.  
XX  
PF 07-JAN-1997; 97EP-0100117.  
XX  
PR 05-JAN-1996; 96US-0009861.  
XX  
XX (HUMA-) HUMAN GENOME SCI INC.  
XX  
XX Barash SC, Choi GH, Dillon PJ, Fannon MR, Kunsch CA;  
PI Rosen CA;  
PI  
XX  
XX WPI; 1997-374922/35.  
DR  
XX  
XX  
XX  
PT Polynucleotide(s) and proteins derived from Staphylococcus aureus -  
PT stored on computer readable medium and used in the production of  
PT anti-S.aureus vaccines  
XX  
PS Claim 1; Page 1526-1527; 3271pp; English.  
XX  
CC This sequence represents one of 5191 Staphylococcus aureus DNA sequences  
CC of the invention. The DNA sequences are recorded on a computer readable  
CC medium, preferably selected from a floppy or hard disk, random access  
CC memory (RAM), read-only memory (ROM) or CD-ROM. Homology searches using  
CC the S.aureus DNA sequences allows putative functions to be assigned so  
CC that protein-encoding or regulatory regions of commercial, therapeutic or  
CC industrial importance can be obtained. Specifically, sequences which are  
CC likely to encode antigens have been identified and these polypeptides can  
CC be used in a vaccine composition against S.aureus infection. The  
CC polypeptides can also be used in a kit for the immunodetection of  
CC S.aureus in a sample. S.aureus is implicated in numerous human diseases,  
CC including cellulitis, eyelid infections, food poisoning, osteomyelitis,  
CC skin and surgical wound infections, scalded skin syndrome, toxic shock  
CC syndrome, etc. Organisms transformed with the DNA sequences can be used  
CC for recombinant production of the polypeptides. The new DNA sequences  
CC (and their fragments) are useful as primers or probes for isolating  
CC homologues of any of the S.aureus DNA sequences contained on the  
CC computer readable medium.  
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SQ Sequence 1393 BP; 448 A; 203 C; 254 G; 426 T; 62 other;

Query Match 12.0%; Score 30; DB 18; Length 1393;  
Best Local Similarity 100.0%; Pred. No. 6.2e-05;  
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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103	28	11.2	87	5	PCT-US96-09472-79	Sequence 79, Appl	176	27	10.8	52	4	US-08-912-951-302	Sequence 302, App
104	28	11.2	87	5	PCT-US96-09537-74	Sequence 74, Appl	177	27	10.8	58	3	US-08-974-549A-536	Sequence 536, App
105	28	11.2	87	5	PCT-US96-09537-186	Sequence 186, App	178	27	10.8	58	4	US-08-912-951-303	Sequence 303, App
106	28	11.2	90	1	US-08-358-995-28	Sequence 28, Appl	179	27	10.8	61	3	US-09-275-850-344	Sequence 344, App
107	28	11.2	90	4	US-09-314-268-177	Sequence 177, App	c 180	27	10.8	61	3	US-09-275-850-345	Sequence 345, App
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124	28	11.2	97	1	US-08-447-172A-1	Sequence 1, Appli	197	27	10.8	72	4	US-08-679-493A-54	Sequence 54, Appl
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144	28	11.2	147	2	US-08-618-700-6	Sequence 6, Appli	c 217	27	10.8	77	1	US-08-412-110-38	Sequence 38, Appl
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164	28	11.2	3083	4	US-09-335-231-25	Sequence 25, Appi	237	27	10.8	77	5	PCT-US95-05600-140	Sequence 140, App
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166	27	10.8	34	4	US-08-974-549A-531	Sequence 531, App	c 239	27	10.8	77	5	PCT-US96-09537-206	Sequence 206, App
167	27	10.8	34	4	US-08-912-951-298	Sequence 298, App	c 240	27	10.8	78	3	US-08-946-138-26	Sequence 26, App
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c 169	27	10.8	39	1	US-08-575-361A-20	Sequence 20, Appl	242	27	10.8	87	1	US-08-243-870-2	Sequence 2, Appli
170	27	10.8	40	3	US-08-974-549A-533	Sequence 533, App	243	27	10.8	87	1	US-08-477-530-1	Sequence 1, Appli
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C 247	27	10.8	87	1	US-08-433-126A-40	Sequence 40, Appl	320	27	10.8	107	5	PCT-US95-05600-18	Sequence 18, Appl
C 248	27	10.8	87	1	US-08-309-245-2	Sequence 2, Appli	C 321	27	10.8	107	5	PCT-US95-05600-21	Sequence 21, Appl
C 249	27	10.8	87	1	US-08-462-389-2	Sequence 2, Appli	C 322	27	10.8	139	4	US-08-679-493A-60	Sequence 60, Appl
C 250	27	10.8	87	1	US-08-458-423A-49	Sequence 49, Appl	323	27	10.8	141	1	US-08-375-116A-131	Sequence 131, App
C 251	27	10.8	87	1	US-08-458-423A-52	Sequence 52, Appl	C 324	27	10.8	142	1	US-08-375-116A-130	Sequence 130, App
C 252	27	10.8	87	1	US-08-458-424B-49	Sequence 49, Appl	C 325	27	10.8	147	2	US-08-618-700-6	Sequence 6, Appli
C 253	27	10.8	87	1	US-08-458-424B-52	Sequence 52, Appl	C 326	27	10.8	147	2	US-08-618-700-7	Sequence 7, Appli
C 254	27	10.8	87	1	US-08-441-828-54	Sequence 54, Appl	C 327	27	10.8	147	2	US-08-618-700-7	Sequence 7, Appli
C 255	27	10.8	87	1	US-08-433-124A-40	Sequence 40, Appl	C 328	27	10.8	147	3	US-09-157-601-6	Sequence 6, Appli
C 256	27	10.8	87	1	US-08-463-101-2	Sequence 2, Appli	C 329	27	10.8	147	3	US-09-157-601-7	Sequence 7, Appli
C 257	27	10.8	87	1	US-08-591-989-12	Sequence 12, Appl	C 330	27	10.8	147	3	US-09-157-601-7	Sequence 7, Appli
C 258	27	10.8	87	2	US-08-488-402A-64	Sequence 64, Appl	C 331	27	10.8	154	2	US-08-721-684C-7	Sequence 7, Appli
C 259	27	10.8	87	2	US-08-488-402A-79	Sequence 79, Appl	C 332	27	10.8	154	2	US-09-005-970-7	Sequence 7, Appli
C 260	27	10.8	87	2	US-08-484-552A-64	Sequence 64, Appl	C 333	27	10.8	154	3	US-09-407-715-7	Sequence 7, Appli
C 261	27	10.8	87	2	US-08-484-552A-79	Sequence 79, Appl	C 334	27	10.8	208	1	US-08-375-116A-132	Sequence 132, App
C 262	27	10.8	87	2	US-08-618-700-2	Sequence 2, Appli	C 335	27	10.8	208	1	US-08-375-116A-132	Sequence 132, App
C 263	27	10.8	87	2	US-08-799-949-2	Sequence 2, Appli	C 336	27	10.8	231	4	US-08-679-493A-13	Sequence 13, Appl
C 264	27	10.8	87	2	US-08-477-527A-74	Sequence 74, Appl	337	27	10.8	252	4	US-09-313-294A-211	Sequence 1788, Ap
C 265	27	10.8	87	2	US-08-477-527A-186	Sequence 74, Appl	338	27	10.8	265	4	US-09-313-294A-211	Sequence 211, App
C 266	27	10.8	87	3	US-08-481-710-74	Sequence 186, App	339	27	10.8	268	4	US-09-313-294A-1104	Sequence 1104, Ap
C 267	27	10.8	87	3	US-08-481-710-186	Sequence 186, App	340	27	10.8	271	4	US-09-313-294A-378	Sequence 378, App
C 268	27	10.8	87	3	US-08-793-398-2	Sequence 2, Appli	341	27	10.8	279	4	US-09-313-294A-3409	Sequence 3409, Ap
C 269	27	10.8	87	3	US-08-793-398-4	Sequence 4, Appli	342	27	10.8	282	4	US-09-313-294A-2238	Sequence 2238, Ap
C 270	27	10.8	87	3	US-09-157-601-2	Sequence 2, Appli	C 343	27	10.8	282	4	US-09-313-294A-4180	Sequence 4180, Ap
C 271	27	10.8	87	3	US-08-976-413A-40	Sequence 40, Appl	344	27	10.8	292	4	US-09-313-294A-811	Sequence 811, App
C 272	27	10.8	87	3	US-08-973-124-49	Sequence 49, Appl	C 345	27	10.8	303	4	US-09-313-294A-5823	Sequence 5823, Ap
C 273	27	10.8	87	3	US-08-973-124-52	Sequence 52, Appl	C 346	27	10.8	305	4	US-09-254-352B-49	Sequence 49, Appl
C 274	27	10.8	87	3	US-09-335-012-44	Sequence 44, Appl	347	27	10.8	305	4	US-09-313-294A-5875	Sequence 5875, Ap
C 275	27	10.8	87	4	US-09-364-539-192	Sequence 192, App	C 348	27	10.8	345	4	US-09-025-203-16	Sequence 16, Appl
C 276	27	10.8	87	4	US-09-941-964-44	Sequence 44, Appl	349	27	10.8	468	3	US-08-821-994-36	Sequence 36, Appl
C 277	27	10.8	87	4	US-10-096-830-44	Sequence 44, Appl	350	27	10.8	493	4	US-09-702-705-13	Sequence 13, Appl
C 278	27	10.8	87	5	PCT-US95-11982-2	Sequence 2, Appli	351	27	10.8	493	4	US-09-736-457-13	Sequence 13, Appl
C 279	27	10.8	87	5	PCT-US95-11982A-2	Sequence 2, Appli	352	27	10.8	495	2	US-08-465-380-31	Sequence 31, Appl
C 280	27	10.8	87	5	PCT-US95-11982A-4	Sequence 4, Appli	353	27	10.8	495	2	US-08-486-397-31	Sequence 31, Appl
C 281	27	10.8	87	5	PCT-US96-06059-40	Sequence 40, Appl	354	27	10.8	495	2	US-08-486-399-31	Sequence 31, Appl
C 282	27	10.8	87	5	PCT-US96-08014-49	Sequence 49, Appl	355	27	10.8	495	2	US-08-461-965-31	Sequence 31, Appl
C 283	27	10.8	87	5	PCT-US96-08014-52	Sequence 52, Appl	C 356	27	10.8	558	2	US-08-647-368A-3	Sequence 3, Appli
C 284	27	10.8	87	5	PCT-US96-09472-64	Sequence 64, Appl	357	27	10.8	750	3	US-08-821-994-40	Sequence 40, Appl
C 285	27	10.8	87	5	PCT-US96-09472-79	Sequence 79, Appl	358	27	10.8	763	4	US-09-484-970B-166	Sequence 166, App
C 286	27	10.8	87	5	PCT-US96-09537-74	Sequence 74, Appl	C 359	27	10.8	808	3	US-09-867-915-27	Sequence 27, Appl
C 287	27	10.8	87	5	PCT-US96-09537-186	Sequence 186, App	360	27	10.8	808	3	US-08-791-115B-12	Sequence 12, Appl
C 288	27	10.8	90	4	US-09-314-268-177	Sequence 177, App	361	27	10.8	808	4	US-09-140-749-23	Sequence 23, Appl
C 289	27	10.8	92	4	US-09-223-139-27	Sequence 27, Appl	C 362	27	10.8	890	4	US-09-016-434-872	Sequence 872, App
C 290	27	10.8	92	4	US-09-223-139-27	Sequence 27, Appl	C 363	27	10.8	897	3	US-09-621-233-1	Sequence 1, Appli
C 291	27	10.8	92	5	PCT-US96-11473A-1	Sequence 1, Appli	C 364	27	10.8	897	4	US-09-724-508-1	Sequence 1, Appli
C 292	27	10.8	92	5	PCT-US96-11473A-1	Sequence 1, Appli	C 365	27	10.8	897	4	US-09-724-516-1	Sequence 1, Appli
C 293	27	10.8	94	4	US-09-364-539-5	Sequence 5, Appli	C 366	27	10.8	1007	4	US-09-328-475C-106	Sequence 106, App
C 294	27	10.8	96	1	US-08-479-783A-36	Sequence 36, Appl	C 367	27	10.8	1024	4	US-09-328-475C-44	Sequence 44, Appl
C 295	27	10.8	96	1	US-08-479-725-36	Sequence 36, Appl	368	27	10.8	1024	4	US-09-328-475C-49	Sequence 49, Appl
C 296	27	10.8	96	1	US-08-618-693-36	Sequence 36, Appl	C 369	27	10.8	1024	4	US-09-328-475C-49	Sequence 49, Appl
C 297	27	10.8	96	3	US-08-973-124-125	Sequence 125, App	C 370	27	10.8	1094	4	US-09-280-116-243	Sequence 243, App
C 298	27	10.8	96	3	US-08-991-743C-36	Sequence 36, Appl	C 371	27	10.8	1233	3	US-09-276-531-7	Sequence 7, Appli
C 299	27	10.8	96	4	US-09-851-486-36	Sequence 36, Appl	C 372	27	10.8	1461	3	US-08-445-463B-5	Sequence 5, Appli
C 300	27	10.8	96	5	PCT-US96-08014-125	Sequence 125, App	C 373	27	10.8	1461	3	US-08-445-464C-5	Sequence 5, Appli
C 301	27	10.8	97	1	US-08-447-172A-1	Sequence 1, Appli	C 374	27	10.8	1461	4	US-08-044-857D-5	Sequence 5, Appli
C 302	27	10.8	97	1	US-08-447-172A-4	Sequence 4, Appli	C 375	27	10.8	1461	5	PCT-US94-03437-5	Sequence 5, Appli
C 303	27	10.8	97	3	US-08-952-793-248	Sequence 248, App	C 376	27	10.8	1474	4	US-09-508-542-17	Sequence 17, Appl
C 304	27	10.8	97	3	US-08-952-793-390	Sequence 390, App	C 377	27	10.8	1474	4	US-09-508-524-17	Sequence 17, Appl
C 305	27	10.8	97	4	US-09-849-928-248	Sequence 248, App	C 378	27	10.8	1576	5	PCT-US95-11405-34	Sequence 34, Appl
C 306	27	10.8	97	4	US-09-849-928-390	Sequence 390, App	C 379	27	10.8	1608	1	US-07-621-670-2	Sequence 2, Appli
C 307	27	10.8	97	5	PCT-US96-09455A-248	Sequence 248, App	380	27	10.8	1738	3	US-09-120-365-89	Sequence 89, Appl
C 308	27	10.8	97	5	PCT-US96-09455A-390	Sequence 390, App	381	27	10.8	1738	3	US-09-515-039-89	Sequence 89, Appl
C 309	27	10.8	99	4	US-08-679-493A-18	Sequence 18, Appl	C 382	27	10.8	2030	4	US-09-484-970B-152	Sequence 152, App
C 310	27	10.8	104	1	US-08-591-989-11	Sequence 11, Appl	C 383	27	10.8	2087	4	US-09-484-970B-153	Sequence 153, App
C 311	27	10.8	104	2	US-08-591-989-1	Sequence 1, Appli	C 384	27	10.8	2475	4	US-09-624-693A-20	Sequence 20, Appl
C 312	27	10.8	104	4	US-09-364-543-1	Sequence 1, Appli	C 385	27	10.8	2635	4	US-09-186-276B-57	Sequence 57, Appl
C 313	27	10.8	104	4	US-09-364-539-191	Sequence 191, App	C 386	27	10.8	2635	4	US-08-842-445-57	Sequence 57, Appl
C 314	27	10.8	107	1	US-08-441-591-1	Sequence 1, Appli	C 387	27	10.8	2635	4	US-09-186-188B-57	Sequence 57, Appl
C 315	27	10.8	107	1	US-08-441-591-4	Sequence 4, Appli	C 388	27	10.8	3083	3	US-08-956-657-1	Sequence 1, Appli
C 316	27	10.8	107	1	US-08-303-362A-1	Sequence 1, Appli	C 389	27	10.8	3083	4	US-09-335-231-25	Sequence 25, Appl
C 317	27	10.8	107	1	US-08-303-362A-4	Sequence 4, Appli	390	27	10.8	3720	1	US-08-074-967-1	Sequence 1, Appli
C 318	27	10.8	107	1	US-08-472-194A-23	Sequence 23, Appl	391	27	10.8	3720	2	US-08-553-541B-1	Sequence 1, Appli
C 319	27	10.8	107	4	US-08-849-567A-23	Sequence 23, Appl	392	27	10.8	3720	3	US-09-268-202-1	Sequence 1, Appli



C 539	26	10.4	80	5	PCT-US96-09455A-126	Sequence 126, App	612	26	10.4	142	1	US-08-375-116A-130	Sequence 130, App
540	26	10.4	81	1	US-08-447-169A-240	Sequence 240, App	C 613	26	10.4	149	3	US-08-903-139B-31	Sequence 31, Appl
C 541	26	10.4	81	1	US-08-447-169A-240	Sequence 240, App	614	26	10.4	150	2	US-08-139-176D-1	Sequence 1, Appli
542	26	10.4	82	4	US-08-679-493A-14	Sequence 14, Appl	615	26	10.4	150	3	US-09-041-841-1	Sequence 1, Appli
543	26	10.4	82	4	US-09-363-939A-9	Sequence 9, Appli	C 616	26	10.4	152	2	US-08-771-201-8	Sequence 8, Appli
C 544	26	10.4	82	4	US-09-363-939A-9	Sequence 9, Appli	C 617	26	10.4	155	3	US-08-903-139B-15	Sequence 15, Appl
545	26	10.4	83	3	US-08-687-421-325	Sequence 325, App	C 618	26	10.4	177	1	US-08-244-116B-18	Sequence 18, Appl
C 546	26	10.4	85	3	US-09-275-850-338	Sequence 338, App	619	26	10.4	184	4	US-09-313-294A-6933	Sequence 6933, Ap
547	26	10.4	85	3	US-09-275-850-339	Sequence 339, App	620	26	10.4	195	4	US-09-186-276B-64	Sequence 64, Appl
548	26	10.4	86	1	US-07-964-624D-43	Sequence 43, Appl	621	26	10.4	195	4	US-08-842-445-64	Sequence 64, Appl
549	26	10.4	86	1	US-08-442-062-43	Sequence 43, Appl	622	26	10.4	195	4	US-09-186-188B-64	Sequence 64, Appl
550	26	10.4	86	1	US-08-748-697A-43	Sequence 43, Appl	C 623	26	10.4	199	4	US-09-186-276B-60	Sequence 60, Appl
551	26	10.4	86	4	US-09-165-616-43	Sequence 43, Appl	C 624	26	10.4	199	4	US-08-842-445-60	Sequence 60, Appl
552	26	10.4	88	4	US-09-363-939A-5	Sequence 5, Appli	C 625	26	10.4	199	4	US-09-186-188B-60	Sequence 60, Appl
C 553	26	10.4	88	4	US-09-363-939A-5	Sequence 5, Appli	626	26	10.4	207	2	US-08-039-198B-6	Sequence 6, Appli
C 554	26	10.4	90	4	US-08-679-493A-17	Sequence 17, Appl	C 627	26	10.4	215	4	US-09-313-294A-6241	Sequence 6241, Ap
C 555	26	10.4	92	4	US-09-301-511A-62	Sequence 62, Appl	628	26	10.4	231	4	US-08-679-493A-13	Sequence 13, Appl
556	26	10.4	93	1	US-08-458-423A-2	Sequence 2, Appli	629	26	10.4	242	4	US-09-313-294A-4646	Sequence 4646, Ap
557	26	10.4	93	1	US-08-458-424B-2	Sequence 2, Appli	630	26	10.4	242	4	US-09-016-434-478	Sequence 478, App
558	26	10.4	93	3	US-08-973-124-2	Sequence 2, Appli	C 631	26	10.4	242	4	US-09-016-434-478	Sequence 478, App
C 559	26	10.4	93	4	US-09-474-432B-1524	Sequence 1524, Ap	632	26	10.4	244	4	US-09-016-434-830	Sequence 830, App
560	26	10.4	93	5	PCT-US96-08014-2	Sequence 2, Appli	C 633	26	10.4	259	3	US-09-103-359-13	Sequence 13, Appl
561	26	10.4	95	1	US-08-458-423A-4	Sequence 4, Appli	C 634	26	10.4	265	4	US-09-313-294A-211	Sequence 211, App
562	26	10.4	95	1	US-08-458-424B-4	Sequence 4, Appli	635	26	10.4	265	4	US-09-313-294A-1611	Sequence 1611, Ap
563	26	10.4	95	3	US-08-973-124-4	Sequence 4, Appli	636	26	10.4	267	4	US-09-107-532A-3091	Sequence 3091, Ap
564	26	10.4	95	5	PCT-US96-08014-4	Sequence 4, Appli	637	26	10.4	268	4	US-09-313-294A-1758	Sequence 1758, Ap
565	26	10.4	96	1	US-08-234-613-1	Sequence 1, Appli	638	26	10.4	269	4	US-09-313-294A-6023	Sequence 6023, Ap
566	26	10.4	96	1	US-08-753-054-19	Sequence 19, Appl	639	26	10.4	270	4	US-09-313-294A-3632	Sequence 3632, Ap
567	26	10.4	96	2	US-08-237-973-1	Sequence 1, Appli	C 640	26	10.4	272	4	US-09-313-294A-435	Sequence 435, App
C 568	26	10.4	98	1	US-08-399-412A-7	Sequence 7, Appli	C 641	26	10.4	275	4	US-09-313-294A-1943	Sequence 1943, Ap
C 569	26	10.4	98	1	US-08-447-172A-28	Sequence 28, Appl	642	26	10.4	277	4	US-09-313-294A-2692	Sequence 2692, Ap
C 570	26	10.4	98	1	US-08-447-172A-31	Sequence 31, Appl	643	26	10.4	278	4	US-09-313-294A-4472	Sequence 4472, Ap
C 571	26	10.4	98	1	US-08-472-255A-1	Sequence 1, Appli	C 644	26	10.4	278	4	US-09-313-294A-4547	Sequence 4547, Ap
C 572	26	10.4	98	1	US-08-479-724A-1	Sequence 1, Appli	645	26	10.4	279	4	US-09-313-294A-100	Sequence 100, App
C 573	26	10.4	98	3	US-08-472-256B-1	Sequence 1, Appli	646	26	10.4	279	4	US-09-313-294A-3975	Sequence 3975, Ap
C 574	26	10.4	98	3	US-08-952-793-1	Sequence 1, Appli	C 647	26	10.4	282	4	US-09-313-294A-6434	Sequence 6434, Ap
575	26	10.4	98	4	US-08-849-567A-50	Sequence 50, Appl	648	26	10.4	282	4	US-09-107-532A-3089	Sequence 3089, Ap
C 576	26	10.4	98	4	US-09-849-928-1	Sequence 1, Appli	649	26	10.4	285	4	US-09-313-294A-6745	Sequence 6745, Ap
C 577	26	10.4	98	5	PCT-US96-09455A-1	Sequence 1, Appli	C 650	26	10.4	286	4	US-09-313-294A-3984	Sequence 3984, Ap
578	26	10.4	99	4	US-08-679-493A-18	Sequence 18, Appl	C 651	26	10.4	287	4	US-09-313-294A-6402	Sequence 6402, Ap
579	26	10.4	99	4	US-08-849-567A-51	Sequence 51, Appl	C 652	26	10.4	288	4	US-09-313-294A-4782	Sequence 4782, Ap
C 580	26	10.4	100	1	US-08-198-670A-2	Sequence 2, Appli	C 653	26	10.4	290	4	US-09-313-294A-6567	Sequence 6567, Ap
C 581	26	10.4	100	5	PCT-US93-09695-2	Sequence 2, Appli	C 654	26	10.4	290	4	US-09-313-294A-6647	Sequence 6647, Ap
C 582	26	10.4	101	1	US-07-843-125-6	Sequence 6, Appli	C 655	26	10.4	291	4	US-09-313-294A-6845	Sequence 6845, Ap
C 583	26	10.4	104	1	US-08-198-670A-36	Sequence 36, Appl	656	26	10.4	292	4	US-09-313-294A-5439	Sequence 5439, Ap
584	26	10.4	104	1	US-08-198-670A-37	Sequence 37, Appl	C 657	26	10.4	292	4	US-09-313-294A-6396	Sequence 6396, Ap
585	26	10.4	104	2	US-08-139-176D-2	Sequence 2, Appli	C 658	26	10.4	293	4	US-09-313-294A-6217	Sequence 6217, Ap
586	26	10.4	104	2	US-08-139-176D-3	Sequence 3, Appli	659	26	10.4	293	4	US-09-313-294A-6465	Sequence 6465, Ap
587	26	10.4	104	3	US-09-041-841-2	Sequence 2, Appli	660	26	10.4	294	4	US-09-313-294A-4086	Sequence 4086, Ap
588	26	10.4	104	3	US-09-041-841-3	Sequence 3, Appli	C 661	26	10.4	294	4	US-09-313-294A-4086	Sequence 4086, Ap
C 589	26	10.4	105	1	US-08-219-012-52	Sequence 52, Appl	662	26	10.4	295	4	US-09-313-294A-5741	Sequence 5741, Ap
C 590	26	10.4	105	3	US-08-687-421-240	Sequence 240, App	663	26	10.4	296	4	US-09-313-294A-4620	Sequence 4620, Ap
C 591	26	10.4	106	1	US-07-843-125-8	Sequence 8, Appli	C 664	26	10.4	297	4	US-09-313-294A-6271	Sequence 6271, Ap
C 592	26	10.4	107	1	US-08-472-194A-23	Sequence 23, Appl	C 665	26	10.4	298	4	US-09-313-294A-5881	Sequence 5881, Ap
593	26	10.4	107	3	US-09-193-068-21	Sequence 21, Appl	C 666	26	10.4	300	4	US-09-313-294A-7389	Sequence 7389, Ap
C 594	26	10.4	107	4	US-08-849-567A-23	Sequence 23, Appl	667	26	10.4	301	4	US-09-313-294A-4954	Sequence 4954, Ap
C 595	26	10.4	108	4	US-09-296-328A-15	Sequence 15, Appl	C 668	26	10.4	304	4	US-09-313-294A-7085	Sequence 7085, Ap
C 596	26	10.4	110	1	US-08-299-498A-3	Sequence 3, Appli	669	26	10.4	305	4	US-09-254-352B-49	Sequence 49, Appl
C 597	26	10.4	110	5	PCT-US95-10813-3	Sequence 3, Appli	C 670	26	10.4	305	4	US-09-313-294A-5875	Sequence 5875, Ap
598	26	10.4	112	1	US-08-299-498A-32	Sequence 32, Appl	671	26	10.4	315	1	US-07-903-466-41	Sequence 41, Appl
599	26	10.4	112	5	PCT-US95-10813-32	Sequence 32, Appl	C 672	26	10.4	315	1	US-07-903-466-41	Sequence 41, Appl
600	26	10.4	117	1	US-08-458-423A-1	Sequence 1, Appli	673	26	10.4	315	5	PCT-US93-05794-41	Sequence 41, Appl
601	26	10.4	117	1	US-08-458-424B-1	Sequence 1, Appli	C 674	26	10.4	315	5	PCT-US93-05794-41	Sequence 41, Appl
602	26	10.4	117	3	US-08-973-124-1	Sequence 1, Appli	675	26	10.4	319	4	US-09-313-294A-5074	Sequence 5074, Ap
603	26	10.4	117	5	PCT-US96-08014-1	Sequence 1, Appli	676	26	10.4	324	2	US-08-378-939-21	Sequence 21, Appl
C 604	26	10.4	119	4	US-08-679-493A-15	Sequence 15, Appl	C 677	26	10.4	324	2	US-08-378-939-27	Sequence 27, Appl
605	26	10.4	122	3	US-09-193-068-16	Sequence 16, Appl	678	26	10.4	345	4	US-09-025-203-16	Sequence 16, Appl
C 606	26	10.4	122	3	US-09-193-068-16	Sequence 16, Appl	C 679	26	10.4	348	4	US-09-672-609-18	Sequence 18, Appl
C 607	26	10.4	132	2	US-08-771-201-7	Sequence 7, Appli	C 680	26	10.4	348	4	US-09-025-403A-18	Sequence 18, Appl
608	26	10.4	134	1	US-08-299-498A-5	Sequence 5, Appli	681	26	10.4	369	4	US-09-107-532A-3090	Sequence 3090, Ap
609	26	10.4	134	5	PCT-US95-10813-5	Sequence 5, Appli	682	26	10.4	414	4	US-09-107-532A-3054	Sequence 3054, Ap
610	26	10.4	137	4	US-09-466-994-2	Sequence 2, Appli	C 683	26	10.4	416	4	US-08-484-841A-13	Sequence 13, Appl
611	26	10.4	139	4	US-08-679-493A-60	Sequence 60, Appl	C 684	26	10.4	423	2	US-08-822-028-62	Sequence 62, Appl



C 685	26	10.4	423	3	US-08-479-285-62	Sequence 62, Appl
C 686	26	10.4	451	4	US-09-582-200A-9	Sequence 9, Appli
C 687	26	10.4	452	4	US-09-582-200A-8	Sequence 8, Appli
C 688	26	10.4	479	4	US-C9-254-352B-39	Sequence 39, Appl
C 689	26	10.4	555	3	US-09-109-205-8	Sequence 8, Appli
C 690	26	10.4	555	4	US-09-495-050A-96	Sequence 96, Appl
C 691	26	10.4	563	3	US-09-276-531-38	Sequence 38, Appl
C 692	26	10.4	595	3	US-09-276-531-63	Sequence 63, Appl
C 693	26	10.4	595	3	US-09-276-531-63	Sequence 63, Appl
C 694	26	10.4	602	4	US-09-334-818A-15	Sequence 15, Appl
C 695	26	10.4	605	3	US-09-109-204-19	Sequence 19, Appl
C 696	26	10.4	605	3	US-09-109-204-19	Sequence 19, Appl
C 697	26	10.4	605	4	US-09-490-032-19	Sequence 19, Appl
C 698	26	10.4	605	4	US-09-490-032-19	Sequence 19, Appl
C 699	26	10.4	608	1	US-08-386-495-11	Sequence 11, Appl
C 700	26	10.4	608	5	PCT-US96-02331-11	Sequence 11, Appl
C 701	26	10.4	616	3	US-09-276-531-39	Sequence 39, Appl
C 702	26	10.4	633	4	US-09-812-484-25	Sequence 25, Appl
C 703	26	10.4	699	3	US-09-276-531-91	Sequence 91, Appl
C 704	26	10.4	729	6	5182210-21	Patent No. 5182210
C 705	26	10.4	759	3	US-09-109-205-11	Sequence 11, Appl
C 706	26	10.4	763	4	US-09-484-970B-166	Sequence 166, App
C 707	26	10.4	789	4	US-09-495-050A-8	Sequence 8, Appli
C 708	26	10.4	804	3	US-09-276-531-54	Sequence 54, Appl
C 709	26	10.4	830	3	US-08-387-707-13	Sequence 13, Appl
C 710	26	10.4	830	3	US-08-387-707-13	Sequence 13, Appl
C 711	26	10.4	830	4	US-08-405-271A-13	Sequence 13, Appl
C 712	26	10.4	830	4	US-08-405-271A-13	Sequence 13, Appl
C 713	26	10.4	869	2	US-08-760-745-2	Sequence 2, Appli
C 714	26	10.4	887	3	US-09-276-531-4	Sequence 4, Appli
C 715	26	10.4	887	3	US-09-276-531-4	Sequence 4, Appli
C 716	26	10.4	915	4	US-09-107-532A-3508	Sequence 3508, Ap
C 717	26	10.4	959	4	US-09-724-510-1	Sequence 1, Appli
C 718	26	10.4	959	4	US-09-723-216-1	Sequence 1, Appli
C 719	26	10.4	959	4	US-09-675-227-1	Sequence 1, Appli
C 720	26	10.4	960	1	US-08-624-125-13	Sequence 13, Appl
C 721	26	10.4	960	1	US-08-624-125-13	Sequence 13, Appl
C 722	26	10.4	960	4	US-08-937-155-13	Sequence 13, Appl
C 723	26	10.4	960	4	US-08-937-155-13	Sequence 13, Appl
C 724	26	10.4	1001	4	US-09-671-317-142	Sequence 142, App
C 725	26	10.4	1070	4	US-09-718-841-3	Sequence 3, Appli
C 726	26	10.4	1070	4	US-09-718-810-3	Sequence 3, Appli
C 727	26	10.4	1083	3	US-09-276-531-30	Sequence 30, Appl
C 728	26	10.4	1143	3	US-09-276-531-103	Sequence 103, App
C 729	26	10.4	1171	4	US-09-636-382A-14	Sequence 14, Appl
C 730	26	10.4	1171	4	US-09-636-382A-14	Sequence 14, Appl
C 731	26	10.4	1183	2	US-08-731-722-8	Sequence 8, Appli
C 732	26	10.4	1238	3	US-09-313-300-10	Sequence 10, Appl
C 733	26	10.4	1252	3	US-09-276-531-92	Sequence 92, Appl
C 734	26	10.4	1457	2	US-08-039-198B-1	Sequence 1, Appli
C 735	26	10.4	1471	2	US-08-039-198B-8	Sequence 8, Appli
C 736	26	10.4	1474	4	US-09-508-542-17	Sequence 17, Appl
C 737	26	10.4	1474	4	US-09-508-524-17	Sequence 17, Appl
C 738	26	10.4	1495	4	US-09-364-230-11	Sequence 11, Appl
C 739	26	10.4	1576	5	PCT-US95-11405-34	Sequence 34, Appl
C 740	26	10.4	1651	4	US-09-484-970B-17	Sequence 17, Appl
C 741	26	10.4	1689	4	US-09-718-841-1	Sequence 1, Appli
C 742	26	10.4	1689	4	US-09-718-810-1	Sequence 1, Appli
C 743	26	10.4	1721	3	US-08-857-213-2	Sequence 2, Appli
C 744	26	10.4	1769	4	US-09-484-970B-46	Sequence 46, Appl
C 745	26	10.4	1769	4	US-09-484-970B-46	Sequence 46, Appl
C 746	26	10.4	1775	2	US-07-862-588B-5	Sequence 5, Appli
C 747	26	10.4	2030	4	US-09-484-970B-152	Sequence 152, App
C 748	26	10.4	2038	3	US-09-276-531-37	Sequence 37, Appl
C 749	26	10.4	2116	2	US-08-653-566A-18	Sequence 18, Appl
C 750	26	10.4	2116	2	US-08-023-610-18	Sequence 18, Appl
C 751	26	10.4	2116	2	US-08-288-065A-18	Sequence 18, Appl
C 752	26	10.4	2116	2	US-08-362-240A-18	Sequence 18, Appl
C 753	26	10.4	2116	5	PCT-US95-10245-18	Sequence 18, Appl
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C 755	26	10.4	2215	3	US-08-891-789B-7	Sequence 7, Appli
C 756	26	10.4	2300	1	US-08-103-998-3	Sequence 3, Appli
C 757	26	10.4	2379	4	US-09-484-970B-139	Sequence 139, App

C 758	26	10.4	2379	4	US-09-484-970B-139	Sequence 139, App
C 759	26	10.4	2428	2	US-08-849-536A-3	Sequence 3, Appli
C 760	26	10.4	2793	1	US-08-209-747-1	Sequence 1, Appli
C 761	26	10.4	2793	1	US-08-458-298-1	Sequence 1, Appli
C 762	26	10.4	2847	4	US-09-484-970B-22	Sequence 22, Appl
C 763	26	10.4	3350	4	US-09-894-998A-48	Sequence 48, Appl
C 764	26	10.4	3450	4	US-09-462-561B-10	Sequence 10, Appl
C 765	26	10.4	3556	3	US-09-276-531-8	Sequence 8, Appli
C 766	26	10.4	3846	2	US-08-845-161A-5	Sequence 5, Appli
C 767	26	10.4	3846	2	US-08-845-161A-5	Sequence 5, Appli
C 768	26	10.4	3846	3	US-09-270-751-5	Sequence 5, Appli
C 769	26	10.4	3846	3	US-09-270-751-5	Sequence 5, Appli
C 770	26	10.4	3846	4	US-09-168-218B-3	Sequence 3, Appli
C 771	26	10.4	3846	4	US-09-168-218B-3	Sequence 3, Appli
C 772	26	10.4	3900	4	US-09-484-970B-27	Sequence 27, Appl
C 773	26	10.4	3915	2	US-08-485-139-6	Sequence 6, Appli
C 774	26	10.4	3915	3	US-08-750-357-6	Sequence 6, Appli
C 775	26	10.4	4339	4	US-09-484-970B-164	Sequence 164, App
C 776	26	10.4	4701	3	US-08-651-472-64	Sequence 64, Appl
C 777	26	10.4	4701	3	US-08-358-928-64	Sequence 64, Appl
C 778	26	10.4	4772	4	US-09-484-970B-133	Sequence 133, App
C 779	26	10.4	4858	4	US-09-392-184-1	Sequence 1, Appli
C 780	26	10.4	4997	1	US-08-232-463-1	Sequence 1, Appli
C 781	26	10.4	5904	1	US-07-745-206A-6	Sequence 6, Appli
C 782	26	10.4	5904	2	US-08-311-363-6	Sequence 6, Appli
C 783	26	10.4	6045	4	US-09-091-501B-7	Sequence 7, Appli
C 784	26	10.4	6775	4	US-09-402-929-4	Sequence 4, Appli
C 785	26	10.4	8299	1	US-08-462-014-2	Sequence 2, Appli
C 786	26	10.4	8299	3	US-08-923-137-3	Sequence 3, Appli
C 787	26	10.4	8299	3	US-08-973-334-5	Sequence 5, Appli
C 788	26	10.4	8299	3	US-09-563-869A-5	Sequence 5, Appli
C 789	26	10.4	8313	1	US-08-232-463-2	Sequence 2, Appli
C 790	26	10.4	8575	5	PCT-US92-08258-6	Sequence 6, Appli
C 791	26	10.4	8575	5	PCT-US92-08258-6	Sequence 6, Appli
C 792	26	10.4	8775	1	US-08-232-463-5	Sequence 5, Appli
C 793	26	10.4	9454	1	US-08-232-463-4	Sequence 3, Appli
C 794	26	10.4	9454	1	US-08-232-463-4	Sequence 3, Appli
C 795	26	10.4	10249	4	US-09-186-002-14	Sequence 14, Appl
C 796	26	10.4	10252	4	US-09-186-002-15	Sequence 15, Appl
C 797	26	10.4	10320	4	US-09-091-501B-9	Sequence 9, Appli
C 798	26	10.4	10339	4	US-09-186-002-13	Sequence 13, Appl
C 799	26	10.4	10785	3	US-08-444-644-27	Sequence 27, Appl
C 800	26	10.4	10785	3	US-08-444-644-27	Sequence 27, Appl
C 801	26	10.4	10785	4	US-08-232-246A-27	Sequence 27, Appl
C 802	26	10.4	10785	4	US-08-232-246A-27	Sequence 27, Appl
C 803	26	10.4	10844	3	US-08-444-644-41	Sequence 41, Appl
C 804	26	10.4	10844	3	US-08-444-644-41	Sequence 41, Appl
C 805	26	10.4	10844	4	US-08-232-246A-41	Sequence 41, Appl
C 806	26	10.4	10844	4	US-08-232-246A-41	Sequence 41, Appl
C 807	26	10.4	11528	3	US-08-444-644-18	Sequence 18, Appl
C 808	26	10.4	11528	4	US-08-232-246A-18	Sequence 18, Appl
C 809	26	10.4	12127	3	US-08-444-644-32	Sequence 32, Appl
C 810	26	10.4	12127	4	US-08-232-246A-32	Sequence 32, Appl
C 811	26	10.4	13977	4	US-09-484-970B-60	Sequence 60, Appl
C 812	26	10.4	15788	4	US-09-920-759-13	Sequence 13, Appl
C 813	26	10.4	15788	4	US-09-920-759-13	Sequence 13, Appl
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C 815	26	10.4	21784	4	US-09-820-002-3	Sequence 3, Appli
C 816	26	10.4	28001	4	US-09-819-993-3	Sequence 3, Appli
C 817	26	10.4	31208	4	US-09-852-067-3	Sequence 3, Appli
C 818	26	10.4	31208	4	US-09-852-067-3	Sequence 3, Appli
C 819	26	10.4	36651	4	US-09-738-894A-3	Sequence 3, Appli
C 820	26	10.4	36651	4	US-09-964-469-3	Sequence 3, Appli
C 821	26	10.4	38564	4	US-09-734-673-3	Sequence 3, Appli
C 822	26	10.4	62804	4	US-09-800-960-3	Sequence 3, Appli
C 823	26	10.4	63588	4	US-09-873-404-3	Sequence 3, Appli
C 824	26	10.4	64467	4	US-09-803-671B-3	Sequence 3, Appli
C 825	26	10.4	65042	4	US-09-784-316-3	Sequence 3, Appli
C 826	26	10.4	74962	4	US-09-685-853A-3	Sequence 3, Appli
C 827	26	10.4	74962	4	US-09-685-853A-3	Sequence 3, Appli
C 828	26	10.4	75395	4	US-09-984-890-3	Sequence 3, Appli
C 829	26	10.4	83450	4	US-09-811-469-3	Sequence 3, Appli
C 830	26	10.4	84495	4	US-09-797-906-3	Sequence 3, Appli



C 831	26	10.4	84495	4	US-09-797-906-3	Sequence 3, Appli	C 904	25	10.0	39	4	US-09-053-116A-2	Sequence 2, Appli
C 832	26	10.4	111282	4	US-09-754-250-3	Sequence 3, Appli	905	25	10.0	40	3	US-09-028-128A-1	Sequence 1, Appli
833	26	10.4	112132	4	US-09-741-150-3	Sequence 3, Appli	C 906	25	10.0	40	3	US-09-028-128A-1	Sequence 1, Appli
C 834	26	10.4	112132	4	US-09-741-150-3	Sequence 3, Appli	C 907	25	10.0	40	3	US-08-974-549A-533	Sequence 533, App
C 835	26	10.4	116592	4	US-09-818-512-3	Sequence 3, Appli	C 908	25	10.0	40	3	US-09-275-850-45	Sequence 45, Appl
C 836	26	10.4	148567	4	US-09-801-876B-3	Sequence 3, Appli	C 909	25	10.0	40	3	US-09-275-850-45	Sequence 45, Appl
837	25	10.0	25	3	US-08-779-355-20	Sequence 20, Appl	C 910	25	10.0	40	3	US-09-275-850-348	Sequence 348, App
C 838	25	10.0	25	3	US-08-779-355-20	Sequence 20, Appl	C 911	25	10.0	40	4	US-08-912-951-300	Sequence 300, App
C 839	25	10.0	25	3	US-08-892-747-8	Sequence 8, Appli	C 912	25	10.0	41	2	US-09-004-192A-9	Sequence 9, Appli
C 840	25	10.0	25	3	US-08-892-747-8	Sequence 8, Appli	C 913	25	10.0	41	2	US-09-004-192A-9	Sequence 9, Appli
C 841	25	10.0	25	3	US-08-938-835A-20	Sequence 20, Appl	C 914	25	10.0	42	2	US-08-659-453B-14	Sequence 14, Appl
C 842	25	10.0	25	3	US-08-938-835A-20	Sequence 20, Appl	C 915	25	10.0	42	3	US-09-089-853A-14	Sequence 14, Appl
C 843	25	10.0	25	4	US-09-004-838-26	Sequence 26, Appl	C 916	25	10.0	42	3	US-09-131-009A-14	Sequence 14, Appl
C 844	25	10.0	25	4	US-09-004-838-26	Sequence 26, Appl	C 917	25	10.0	42	3	US-09-092-226A-14	Sequence 14, Appl
C 845	25	10.0	25	4	US-07-868-539C-18	Sequence 18, Appl	C 918	25	10.0	42	3	US-09-130-862A-14	Sequence 14, Appl
C 846	25	10.0	25	4	US-07-868-539C-18	Sequence 18, Appl	C 919	25	10.0	42	3	US-09-090-809A-14	Sequence 14, Appl
C 847	25	10.0	28	1	US-07-976-103A-50	Sequence 50, Appl	C 920	25	10.0	42	4	US-08-679-493A-55	Sequence 55, Appl
C 848	25	10.0	28	1	US-07-976-103A-50	Sequence 50, Appl	C 921	25	10.0	42	4	US-09-053-116A-14	Sequence 14, Appl
C 849	25	10.0	28	2	US-08-473-481-50	Sequence 50, Appl	C 922	25	10.0	43	3	US-09-275-850-44	Sequence 44, Appl
C 850	25	10.0	28	2	US-08-473-481-50	Sequence 50, Appl	C 923	25	10.0	43	3	US-09-275-850-44	Sequence 44, Appl
C 851	25	10.0	28	3	US-08-779-355-21	Sequence 21, Appl	C 924	25	10.0	44	2	US-08-659-453B-22	Sequence 22, Appl
C 852	25	10.0	28	3	US-08-779-355-21	Sequence 21, Appl	C 925	25	10.0	44	2	US-08-659-453B-22	Sequence 22, Appl
C 853	25	10.0	28	3	US-08-938-835A-21	Sequence 21, Appl	C 926	25	10.0	44	3	US-09-089-853A-22	Sequence 22, Appl
C 854	25	10.0	28	3	US-08-938-835A-21	Sequence 21, Appl	C 927	25	10.0	44	3	US-09-131-009A-22	Sequence 22, Appl
C 855	25	10.0	28	4	US-08-599-738A-50	Sequence 50, Appl	C 928	25	10.0	44	3	US-09-092-226A-22	Sequence 22, Appl
C 856	25	10.0	28	4	US-08-599-738A-50	Sequence 50, Appl	C 929	25	10.0	44	3	US-09-130-862A-22	Sequence 22, Appl
C 857	25	10.0	29	1	US-08-162-590A-1	Sequence 1, Appli	C 930	25	10.0	44	3	US-09-090-809A-22	Sequence 22, Appl
C 858	25	10.0	29	1	US-08-162-590A-1	Sequence 1, Appli	C 931	25	10.0	44	4	US-09-053-116A-22	Sequence 22, Appl
C 859	25	10.0	29	1	US-08-162-590A-2	Sequence 2, Appli	C 932	25	10.0	45	3	US-08-180-470-76	Sequence 76, Appl
C 860	25	10.0	29	1	US-08-162-590A-2	Sequence 2, Appli	C 933	25	10.0	46	3	US-08-974-549A-534	Sequence 534, App
C 861	25	10.0	29	1	US-08-162-590A-3	Sequence 3, Appli	C 934	25	10.0	46	4	US-08-912-951-301	Sequence 301, App
C 862	25	10.0	29	1	US-08-162-590A-3	Sequence 3, Appli	C 935	25	10.0	46	4	US-09-301-721A-1	Sequence 1, Appli
C 863	25	10.0	29	1	US-08-372-556-8	Sequence 8, Appli	C 936	25	10.0	47	4	US-09-301-721A-2	Sequence 2, Appli
C 864	25	10.0	29	1	US-08-372-556-8	Sequence 8, Appli	C 937	25	10.0	47	2	US-08-769-945C-7	Sequence 7, Appli
C 865	25	10.0	29	1	US-08-372-556-7	Sequence 7, Appli	C 938	25	10.0	47	2	US-08-769-945C-8	Sequence 8, Appli
C 866	25	10.0	30	1	US-08-372-556-7	Sequence 7, Appli	C 939	25	10.0	47	2	US-08-769-945C-8	Sequence 8, Appli
C 867	25	10.0	30	3	US-08-892-747-7	Sequence 7, Appli	940	25	10.0	50	1	US-07-931-473B-54	Sequence 54, Appl
C 868	25	10.0	30	3	US-08-892-747-7	Sequence 7, Appli	C 941	25	10.0	50	1	US-07-931-473B-54	Sequence 54, Appl
C 869	25	10.0	30	4	US-09-083-123-6	Sequence 6, Appli	942	25	10.0	50	1	US-07-714-131C-54	Sequence 54, Appl
C 870	25	10.0	30	4	US-09-083-123-6	Sequence 6, Appli	C 943	25	10.0	50	1	US-07-714-131C-54	Sequence 54, Appl
C 871	25	10.0	33	1	US-08-162-590A-9	Sequence 9, Appli	C 944	25	10.0	50	1	US-08-412-110-54	Sequence 54, Appl
C 872	25	10.0	33	1	US-08-162-590A-9	Sequence 9, Appli	C 945	25	10.0	50	1	US-08-412-110-54	Sequence 54, Appl
C 873	25	10.0	33	1	US-08-162-590A-10	Sequence 10, Appl	946	25	10.0	50	1	US-08-409-442A-54	Sequence 54, Appl
C 874	25	10.0	33	1	US-08-162-590A-10	Sequence 10, Appl	C 947	25	10.0	50	1	US-08-409-442A-54	Sequence 54, Appl
C 875	25	10.0	34	3	US-08-974-549A-531	Sequence 531, App	C 948	25	10.0	50	1	US-08-409-442A-54	Sequence 54, Appl
C 876	25	10.0	34	3	US-08-974-549A-532	Sequence 532, App	C 949	25	10.0	50	1	US-08-409-442A-353	Sequence 353, App
C 877	25	10.0	34	3	US-08-974-549A-532	Sequence 532, App	950	25	10.0	50	2	US-08-469-609A-54	Sequence 54, Appl
C 878	25	10.0	34	4	US-09-364-539-11	Sequence 11, Appl	C 951	25	10.0	50	2	US-08-469-609A-54	Sequence 54, Appl
C 879	25	10.0	34	4	US-09-364-539-11	Sequence 11, Appl	C 952	25	10.0	50	2	US-08-469-609A-353	Sequence 353, App
C 880	25	10.0	34	4	US-08-912-951-298	Sequence 298, App	C 953	25	10.0	50	2	US-08-469-609A-353	Sequence 353, App
C 881	25	10.0	34	4	US-08-912-951-299	Sequence 299, App	954	25	10.0	50	3	US-09-143-190-54	Sequence 54, Appl
C 882	25	10.0	34	4	US-08-912-951-299	Sequence 299, App	C 955	25	10.0	50	3	US-09-143-190-54	Sequence 54, Appl
C 883	25	10.0	37	1	US-08-162-590A-5	Sequence 5, Appli	C 956	25	10.0	50	3	US-09-143-190-353	Sequence 353, App
C 884	25	10.0	37	1	US-08-162-590A-5	Sequence 5, Appli	C 957	25	10.0	50	3	US-09-143-190-353	Sequence 353, App
C 885	25	10.0	37	1	US-08-162-590A-6	Sequence 6, Appli	C 958	25	10.0	50	3	US-09-593-323-26	Sequence 26, Appl
C 886	25	10.0	37	1	US-08-162-590A-6	Sequence 6, Appli	C 959	25	10.0	50	3	US-09-593-323-26	Sequence 26, Appl
C 887	25	10.0	37	1	US-08-162-590A-7	Sequence 7, Appli	960	25	10.0	50	3	US-09-594-108-26	Sequence 26, Appl
C 888	25	10.0	37	1	US-08-162-590A-7	Sequence 7, Appli	C 961	25	10.0	50	3	US-09-594-108-26	Sequence 26, Appl
C 889	25	10.0	37	1	US-08-162-590A-8	Sequence 8, Appli	962	25	10.0	50	3	US-09-344-300-26	Sequence 26, Appl
C 890	25	10.0	37	1	US-08-162-590A-8	Sequence 8, Appli	C 963	25	10.0	50	3	US-09-344-300-26	Sequence 26, Appl
C 891	25	10.0	38	3	US-09-275-850-336	Sequence 336, App	964	25	10.0	50	4	US-09-502-344-54	Sequence 54, Appl
C 892	25	10.0	38	3	US-09-275-850-336	Sequence 336, App	C 965	25	10.0	50	4	US-09-502-344-54	Sequence 54, Appl
C 893	25	10.0	38	3	US-09-275-850-337	Sequence 337, App	966	25	10.0	50	4	US-09-502-344-353	Sequence 353, App
C 894	25	10.0	38	3	US-09-275-850-337	Sequence 337, App	C 967	25	10.0	50	4	US-09-502-344-353	Sequence 353, App
C 895	25	10.0	39	1	US-08-575-361A-19	Sequence 19, Appl	968	25	10.0	51	3	US-09-275-850-179	Sequence 179, App
C 896	25	10.0	39	1	US-08-575-361A-20	Sequence 20, Appl	C 969	25	10.0	51	3	US-09-275-850-179	Sequence 179, App
C 897	25	10.0	39	2	US-08-659-453B-2	Sequence 2, Appli	C 970	25	10.0	52	3	US-08-974-549A-535	Sequence 535, App
C 898	25	10.0	39	3	US-09-089-853A-2	Sequence 2, Appli	C 971	25	10.0	52	4	US-08-912-951-302	Sequence 302, App
C 899	25	10.0	39	3	US-09-131-009A-2	Sequence 2, Appli	972	25	10.0	52	4	US-09-916-228-29	Sequence 29, Appl
C 900	25	10.0	39	3	US-09-092-226A-2	Sequence 2, Appli	C 973	25	10.0	52	4	US-09-916-228-29	Sequence 29, Appl
C 901	25	10.0	39	3	US-09-130-862A-2	Sequence 2, Appli	974	25	10.0	54	4	US-09-504-132-9	Sequence 9, Appli
C 902	25	10.0	39	3	US-09-275-850-340	Sequence 340, App	975	25	10.0	55	3	US-09-275-850-333	Sequence 333, App
C 903	25	10.0	39	3	US-09-090-809A-2	Sequence 2, Appli	C 976	25	10.0	55	3	US-09-275-850-333	Sequence 333, App

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977      25 10.0 55 3 US-09-275-850-334      Sequence 334, App
c 978      25 10.0 55 3 US-09-275-850-334      Sequence 334, App
979      25 10.0 55 3 US-09-275-850-335      Sequence 335, App
c 980      25 10.0 55 3 US-09-275-850-335      Sequence 335, App
981      25 10.0 56 2 US-08-432-871C-3       Sequence 3, Appli
c 982      25 10.0 56 2 US-08-432-871C-3       Sequence 3, Appli
983      25 10.0 56 4 US-09-270-956-3       Sequence 3, Appli
c 984      25 10.0 56 4 US-09-270-956-3       Sequence 3, Appli
985      25 10.0 57 2 US-08-136-214-8       Sequence 8, Appli
c 986      25 10.0 57 2 US-08-136-214-8       Sequence 8, Appli
987      25 10.0 58 3 US-08-974-549A-536     Sequence 536, App
c 988      25 10.0 58 4 US-08-912-951-303     Sequence 303, App
c 989      25 10.0 59 1 US-07-964-624D-13     Sequence 13, Appl
c 990      25 10.0 59 1 US-08-442-062-13     Sequence 13, Appl
991      25 10.0 60 2 US-09-004-192A-11     Sequence 11, Appl
c 992      25 10.0 60 2 US-09-004-192A-11     Sequence 11, Appl
c 993      25 10.0 60 3 US-09-150-805-1       Sequence 1, Appli
c 994      25 10.0 60 3 US-08-996-069A-1       Sequence 1, Appli
c 995      25 10.0 60 4 US-09-083-123-1       Sequence 1, Appli
996      25 10.0 61 2 US-08-792-075-1       Sequence 1, Appli
c 997      25 10.0 61 2 US-08-792-075-1       Sequence 1, Appli
998      25 10.0 61 3 US-09-046-247-2       Sequence 2, Appli
c 999      25 10.0 61 3 US-09-046-247-2       Sequence 2, Appli
1000     25 10.0 61 3 US-08-870-930-10       Sequence 10, Appl

ALIGNMENTS

RESULT 1
US-08-837-199A-21/c
; Sequence 21, Application US/08837199A
; Patent No. 6455277
; GENERAL INFORMATION:
; APPLICANT: FOX, GARY M.
; APPLICANT: JING, SHUQIAN
; APPLICANT: WEN, DUANZHI
; TITLE OF INVENTION: GLIAL CELL LINE-DERIVED NEUROTROPHIC FACTOR RECEPTOR
; FILE REFERENCE: A-401C
; CURRENT FILING DATE: 1997-04-14
; PRIOR APPLICATION NUMBER: US/08/837,199A
; PRIOR FILING DATE: 1996-04-22
; PRIOR APPLICATION NUMBER: US 60/015,907
; PRIOR FILING DATE: 1996-04-22
; PRIOR APPLICATION NUMBER: US 60/017,221
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 21
; LENGTH: 1075
; TYPE: DNA
; ORGANISM: HUMAN
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (2)..(445)
; OTHER INFORMATION:
; NAME/KEY: misc_feature
; LOCATION: (1)..(1075)
; OTHER INFORMATION: No. 6455277e= "1 to 1075 is 1255 to 2330 of Figure 5 Hsgr-2"
; NAME/KEY: misc_feature
; LOCATION: (763)..(801)
; OTHER INFORMATION: N in position 763 to 801 indicates positions of divergence between
; OTHER INFORMATION: n different receptor clones.
JS-08-837-199A-21

Query Match      12.4%; Score 31; DB 4; Length 1075;
Best Local Similarity 100.0%; Pred. No. 4.6e-07;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

2y      94 AAAATCNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 124
      |||||||
db      807 AAAATCNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 777


```

```

RESULT 2
US-08-837-199A-46/c
; Sequence 46, Application US/08837199A
; Patent No. 6455277
; GENERAL INFORMATION:
; APPLICANT: FOX, GARY M.
; APPLICANT: JING, SHUQIAN
; APPLICANT: WEN, DUANZHI
; TITLE OF INVENTION: GLIAL CELL LINE-DERIVED NEUROTROPHIC FACTOR RECEPTOR
; FILE REFERENCE: A-401C
; CURRENT APPLICATION NUMBER: US/08/837,199A
; CURRENT FILING DATE: 1997-04-14
; PRIOR APPLICATION NUMBER: US 60/015,907
; PRIOR FILING DATE: 1996-04-22
; PRIOR APPLICATION NUMBER: US 60/017,221
; PRIOR FILING DATE: 1996-05-09
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 46
; LENGTH: 1076
; TYPE: DNA
; ORGANISM: HUMAN
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (586)..(586)
; OTHER INFORMATION: N in position 586 indicates a position of divergence between di
; OTHER INFORMATION: erent receptor clones.
; NAME/KEY: misc_feature
; LOCATION: (764)..(802)
; OTHER INFORMATION: N in positions 764 to 802 indicates positions of divergence be
; OTHER INFORMATION: een different receptor clones.
US-08-837-199A-46

Query Match      12.4%; Score 31; DB 4; Length 1076;
Best Local Similarity 100.0%; Pred. No. 4.6e-07;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      94 AAAATCNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 124
      |||||||
Db      808 AAAATCNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 778

RESULT 3
US-08-837-199A-15/c
; Sequence 15, Application US/08837199A
; Patent No. 6455277
; GENERAL INFORMATION:
; APPLICANT: FOX, GARY M.
; APPLICANT: JING, SHUQIAN
; APPLICANT: WEN, DUANZHI
; TITLE OF INVENTION: GLIAL CELL LINE-DERIVED NEUROTROPHIC FACTOR RECEPTOR
; FILE REFERENCE: A-401C
; CURRENT APPLICATION NUMBER: US/08/837,199A
; CURRENT FILING DATE: 1997-04-14
; PRIOR APPLICATION NUMBER: US 60/015,907
; PRIOR FILING DATE: 1996-04-22
; PRIOR APPLICATION NUMBER: US 60/017,221
; PRIOR FILING DATE: 1996-05-09
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 15
; LENGTH: 2157
; TYPE: DNA
; ORGANISM: HUMAN
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (2)..(886)
; OTHER INFORMATION:
; NAME/KEY: misc_feature
; LOCATION: (1)..(2157)
; OTHER INFORMATION: No. 6455277e= "1 to 2157 is 814 to 2971 of Figure 5 29brc"
; NAME/KEY: misc_feature
; LOCATION: (1204)..(1242)

```



OTHER INFORMATION: N in position 2078 indicates a position of divergence between dif  
OTHER INFORMATION: ferent receptor clones  
NAME/KEY: misc feature  
LOCATION: (2256)..(2294)  
OTHER INFORMATION: N in positions 2256 to 2294 indicates positions of divergence bet  
OTHER INFORMATION: ween different receptor clones  
NAME/KEY: misc feature  
LOCATION: (1091)..(1091)  
OTHER INFORMATION: N in position 1091 indicates any nucleic acid  
US-08-837-199A-5

Query Match 12.4%; Score 31; DB 4; Length 3209;  
Best Local Similarity 100.0%; Pred. No. 4.4e-07;  
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 94 AAAATCNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 124  
|||||  
DB 2300 AAAATCNNNNNNNNNNNNNNNNNNNNNNNNNNNN 2270

RESULT 7  
US-08-837-199A-37/c  
Sequence 37, Application US/08837199A  
Patent No. 6455277  
GENERAL INFORMATION:  
APPLICANT: FOX, GARY M.  
APPLICANT: JING, SHUQIAN  
APPLICANT: WEN, DUANZHI  
TITLE OF INVENTION: GLIAL CELL LINE-DERIVED NEUROTROPHIC FACTOR RECEPTOR  
FILE REFERENCE: A-401C  
CURRENT APPLICATION NUMBER: US/08/837,199A  
CURRENT FILING DATE: 1997-04-14  
PRIOR APPLICATION NUMBER: US 60/015,907  
PRIOR FILING DATE: 1996-04-22  
PRIOR APPLICATION NUMBER: US 60/017,221  
PRIOR FILING DATE: 1996-05-09  
NUMBER OF SEQ ID NOS: 47  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 37  
LENGTH: 3209  
TYPE: DNA  
ORGANISM: HUMAN  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: (1091)..(1091)  
OTHER INFORMATION: N in position 1091 indicates any nucleic acid.

NAME/KEY: misc feature  
LOCATION: (2078)..(2078)  
OTHER INFORMATION: N in position 2078 indicates a position of divergence between dif  
OTHER INFORMATION: ferent receptor clones.  
NAME/KEY: misc feature  
LOCATION: (2256)..(2294)  
OTHER INFORMATION: N in positions 2256 to 2294 indicates positions of divergence bet  
OTHER INFORMATION: ween different receptor clones.  
US-08-837-199A-37

Query Match 12.4%; Score 31; DB 4; Length 3209;  
Best Local Similarity 100.0%; Pred. No. 4.4e-07;  
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 94 AAAATCNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 124  
|||||  
DB 2300 AAAATCNNNNNNNNNNNNNNNNNNNNNNNNNNNN 2270

RESULT 8  
JS-09-867-915-27  
Sequence 27, Application US/09867915  
Patent No. 6521747  
GENERAL INFORMATION:  
APPLICANT: Genaisance Pharmaceuticals, Inc.  
APPLICANT: Anastasio, Alison E.  
APPLICANT: Finkel, Kevin

APPLICANT: Koshy, Beena  
APPLICANT: Lee, Helen H.  
TITLE OF INVENTION: HAPLOTYPES OF THE AGTR1 GENE  
FILE REFERENCE: AGTR1-1136test  
CURRENT APPLICATION NUMBER: US/09/867,915  
CURRENT FILING DATE: 2001-05-30  
PRIOR APPLICATION NUMBER: 60/228,542  
PRIOR FILING DATE: 2000-08-28  
NUMBER OF SEQ ID NOS: 27  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 27  
LENGTH: 780  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: allele  
LOCATION: (30)  
OTHER INFORMATION: PS1: polymorphic base T or A  
NAME/KEY:  
LOCATION: (61)..(120)  
OTHER INFORMATION: nucleotides represent sequence between PS  
NAME/KEY: allele  
LOCATION: (150)  
OTHER INFORMATION: PS2: polymorphic base G or T  
NAME/KEY:  
LOCATION: (181)..(240)  
OTHER INFORMATION: nucleotides represent sequence between PS  
NAME/KEY: allele  
LOCATION: (270)  
OTHER INFORMATION: PS3: polymorphic base T or C  
NAME/KEY:  
LOCATION: (301)..(360)  
OTHER INFORMATION: nucleotides represent sequence between PS  
NAME/KEY: allele  
LOCATION: (390)  
OTHER INFORMATION: PS4: polymorphic base T or C  
NAME/KEY:  
LOCATION: (421)..(480)  
OTHER INFORMATION: nucleotides represent sequence between PS  
NAME/KEY: allele  
LOCATION: (510)  
OTHER INFORMATION: PS5: polymorphic base C or T  
NAME/KEY:  
LOCATION: (541)..(600)  
OTHER INFORMATION: nucleotides represent sequence between PS  
NAME/KEY: allele  
LOCATION: (630)  
OTHER INFORMATION: PS6: polymorphic base A or G  
NAME/KEY:  
LOCATION: (661)..(720)  
OTHER INFORMATION: nucleotides represent sequence between PS  
NAME/KEY: allele  
LOCATION: (750)  
OTHER INFORMATION: PS7: polymorphic base T or G  
US-09-867-915-27

Query Match 12.0%; Score 30; DB 4; Length 780;  
Best Local Similarity 100.0%; Pred. No. 1.6e-06;  
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 100 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNTTCCA 129  
|||||  
DB 216 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNTTCCA 245

RESULT 9  
US-09-484-970B-26/c  
Sequence 26, Application US/09484970B  
Patent No. 6426186  
GENERAL INFORMATION:  
APPLICANT: Jones, Karen A.  
APPLICANT: Volkmuth, Wayne  
APPLICANT: Walker, Michael G.



TITLE OF INVENTION: BONE REMODELING GENES  
FILE REFERENCE: PB-0014 US  
CURRENT APPLICATION NUMBER: US/09/484,970B  
CURRENT FILING DATE: 2000-01-18  
NUMBER OF SEQ ID NOS: 172  
SOFTWARE: PERL Program  
SEQ ID NO 26  
LENGTH: 3017  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: misc feature  
OTHER INFORMATION: incyte ID No. 6426186 232773.2CB1  
NAME/KEY: unsure  
LOCATION: 1463-1495  
OTHER INFORMATION: a, t, c, g, or other

JS-09-484-970B-26

Query Match 12.0%; Score 30; DB 4; Length 3017;  
Best Local Similarity 100.0%; Pred. No. 1.5e-06;  
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

NY 95 AAATCNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 124  
|||||  
b 1500 AAATCNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 1471

ESULT 10

S-08-679-493A-55  
Sequence 55, Application US/08679493A  
Patent No. 6303295  
GENERAL INFORMATION:  
APPLICANT: Taylor, Ethan W.  
TITLE OF INVENTION: SELENOPROTEINS, CODING SEQUENCES AND METHODS  
FILE REFERENCE: 55-95  
CURRENT APPLICATION NUMBER: US/08/679,493A  
CURRENT FILING DATE: 1996-07-12  
PRIOR APPLICATION NUMBER: 60/001203  
PRIOR FILING DATE: 1995-07-14  
PRIOR APPLICATION NUMBER: 60/003,112  
PRIOR FILING DATE: 1995-09-01  
NUMBER OF SEQ ID NOS: 216  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 55  
LENGTH: 42  
TYPE: RNA  
ORGANISM: Human immunodeficiency virus type 1  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: (1)..(42)  
OTHER INFORMATION: N is A, U, G or C.

S-08-679-493A-55

Query Match 11.6%; Score 29; DB 4; Length 42;  
Best Local Similarity 93.1%; Pred. No. 5.8e-06;  
Matches 27; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

NY 100 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNTTCC 128  
|||||  
b 9 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNUUCC 37

ESULT 11

S-09-313-300-9/c  
Sequence 9, Application US/09313300  
Patent No. 622027  
GENERAL INFORMATION:  
APPLICANT: Kaser, Matthew, R.  
APPLICANT: Lal, Preeti  
APPLICANT: Yue, Henry  
APPLICANT: Tang, Tom, Y.  
APPLICANT: Baughn, Mariah, R.  
APPLICANT: Azimzai, Yalda

TITLE OF INVENTION: MOLECULES EXPRESSED IN HIPPOCAMPUS  
FILE REFERENCE: PB-0012 US  
CURRENT APPLICATION NUMBER: US/09/313,300  
CURRENT FILING DATE: 1999-05-17  
NUMBER OF SEQ ID NOS: 15  
SOFTWARE: PERL Program  
SEQ ID NO 9  
LENGTH: 1045  
TYPE: DNA  
ORGANISM: Rattus norvegicus  
FEATURE:  
NAME/KEY: unsure  
LOCATION: (871)...(899)  
OTHER INFORMATION: a or g or c or t, unknown, or other  
FEATURE:  
NAME/KEY:  
OTHER INFORMATION: 700122146  
PUBLICATION INFORMATION:  
US-09-313-300-9

Query Match 11.6%; Score 29; DB 3; Length 1045;  
Best Local Similarity 100.0%; Pred. No. 5.1e-06;  
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 100 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNTTCC 128  
|||||  
Db 895 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNTTCC 867

RESULT 12

US-08-444-644-24/c  
Sequence 24, Application US/08444644  
Patent No. 601555  
GENERAL INFORMATION:  
APPLICANT: Friden, Phillip M.  
TITLE OF INVENTION: TRANSFERRIN RECEPTOR SPECIFIC  
TITLE OF INVENTION: ANTIBODY-NEUROPHARMACEUTICAL OR DIAGNOSTIC AGENT  
TITLE OF INVENTION: CONJUGATES  
NUMBER OF SEQUENCES: 46  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.  
STREET: Two Militia Drive  
CITY: Lexington  
STATE: MA  
COUNTRY: USA  
ZIP: 02173  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC Compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/444,644  
FILING DATE:  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/232,246  
FILING DATE: 07-JUL-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/800,458  
FILING DATE: 26-NOV-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US90/05077  
FILING DATE: 07-SEP-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/404,089  
FILING DATE: 07-SEP-1989  
ATTORNEY/AGENT INFORMATION:  
NAME: Wagner, Richard W.  
REGISTRATION NUMBER: 34,480  
REFERENCE/DOCKET NUMBER: ALK88-15AAAZ  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 861-6240

```

; TELEFAX: (617) 861-9540
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13999 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: circular
; MOLECULE TYPE: DNA (genomic)
; IMMEDIATE SOURCE:
; CLONE: PAG4611
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 1..13999
; OTHER INFORMATION: /note= "Function = "Expression
; OTHER INFORMATION: Vector Coding Sequence"
US-08-444-644-24

Query Match 11.6%; Score 29; DB 3; Length 13999;
Best Local Similarity 100.0%; Pred. No. 4.7e-06;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 96 AATCANNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 124
Db 11461 AATCANNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 11433

RESULT 13
JS-08-232-246A-24/c
Sequence 24, Application US/08232246A
Patent No. 6329508
; GENERAL INFORMATION:
; APPLICANT: Friden, Phillip M.
; TITLE OF INVENTION: TRANSFERRIN RECEPTOR SPECIFIC
; TITLE OF INVENTION: ANTIBODY-NEUROPHARMACEUTICAL OR DIAGNOSTIC AGENT
; TITLE OF INVENTION: CONJUGATES
; NUMBER OF SEQUENCES: 46
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: MA
; COUNTRY: USA
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,246A
FILING DATE: 04-MAY-1994
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/600,458
FILING DATE: 26-NOV-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US90/05077
FILING DATE: 07-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/404,089
FILING DATE: 07-SEP-1989
ATTORNEY/AGENT INFORMATION:
NAME: Wagner, Richard W.
REGISTRATION NUMBER: 34,480
REFERENCE/DOCKET NUMBER: ALK88-15AAA
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 861-6240
TELEFAX: (617) 861-9540
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 13999 base pairs
TYPE: nucleic acid
STRANDEDNESS: double

```

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; TOPOLOGY: circular
; MOLECULE TYPE: DNA (genomic)
; IMMEDIATE SOURCE:
; CLONE: PAG4611
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 1..13999
; OTHER INFORMATION: /note= "Function = "Expression
; OTHER INFORMATION: Vector Coding Sequence"
US-08-232-246A-24

Query Match 11.6%; Score 29; DB 4; Length 13999;
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RESULT 14
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Sequence 3, Application US/09804471A
Patent No. 6479269
; GENERAL INFORMATION:
; APPLICANT: WEBSTER, Marion et al
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL001164
; CURRENT APPLICATION NUMBER: US/09/804,471A
; CURRENT FILING DATE: 2001-03-13
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 174493
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc feature
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; OTHER INFORMATION: n = A,T,C or G
US-09-804-471A-3

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RESULT 15
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Sequence 31, Application US/09645629
Patent No. 6472515
; GENERAL INFORMATION:
; APPLICANT: Climent-Johansson, Isabel
; APPLICANT: Dahlman-Wright, Karin
; APPLICANT: Lake, Staffan
; APPLICANT: Wasserman, Wyeth
; TITLE OF INVENTION: NOVEL RESPONSE ELEMENT
; FILE REFERENCE: 13425-032001
; CURRENT APPLICATION NUMBER: US/09/645,629
; CURRENT FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: SE 9904269-9
; PRIOR FILING DATE: 1999-11-25
; PRIOR APPLICATION NUMBER: US 60/151,867
; PRIOR FILING DATE: 1999-08-31
; PRIOR APPLICATION NUMBER: SE 9903009-0
; PRIOR FILING DATE: 1999-08-26
; NUMBER OF SEQ ID NOS: 34

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; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 31
; LENGTH: 65
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: oligonucleotide for DNA binding site selection
; NAME/KEY: misc feature
; LOCATION: (1)..(65)
; OTHER INFORMATION: n = A,T,C or G
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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: November 6, 2003, 04:14:30 ; Search time 1046 Seconds  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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C 292	27	10.8	51	14	US-10-224-836-73	Sequence 5, Appli
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C 296	27	10.8	52	14	US-10-044-539-302	Sequence 75, Appl
C 297	27	10.8	53	14	US-10-224-836-75	Sequence 76, Appl
C 298	27	10.8	54	14	US-10-224-836-76	Sequence 77, Appl
C 299	27	10.8	55	14	US-10-224-836-77	Sequence 78, Appl
C 300	27	10.8	56	14	US-10-224-836-78	Sequence 79, Appl
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C 302	27	10.8	58	14	US-10-224-836-80	Sequence 303, App
C 303	27	10.8	58	14	US-10-044-692-303	Sequence 303, App
C 304	27	10.8	58	14	US-10-044-539-303	Sequence 81, Appl
C 305	27	10.8	59	14	US-10-224-836-81	Sequence 124, App
C 306	27	10.8	60	12	US-10-269-031A-124	Sequence 82, Appl
C 307	27	10.8	60	14	US-10-224-836-82	Sequence 344, App
C 308	27	10.8	61	11	US-09-907-111-344	

C 309	27	10.8	61	11	US-09-907-111-345	Sequence 345, App
C 310	27	10.8	61	14	US-10-224-836-83	Sequence 83, Appl
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C 312	27	10.8	63	14	US-10-224-836-85	Sequence 85, Appl
C 313	27	10.8	64	14	US-10-224-836-86	Sequence 86, Appl
C 314	27	10.8	65	8	US-08-681-219-35	Sequence 35, Appl
C 315	27	10.8	65	12	US-10-092-138-33	Sequence 33, Appl
C 316	27	10.8	65	12	US-09-230-111C-33	Sequence 33, Appl
C 317	27	10.8	65	14	US-10-224-836-87	Sequence 87, Appl
C 318	27	10.8	66	9	US-09-766-113-9	Sequence 9, Appli
C 319	27	10.8	66	14	US-10-224-836-88	Sequence 88, Appl
C 320	27	10.8	67	14	US-10-224-836-89	Sequence 89, Appl
C 321	27	10.8	68	14	US-10-224-836-90	Sequence 90, Appl
C 322	27	10.8	69	12	US-10-164-915-4	Sequence 4, Appli
C 323	27	10.8	69	14	US-10-224-836-91	Sequence 91, Appl
C 324	27	10.8	70	14	US-10-224-836-92	Sequence 92, Appl
C 325	27	10.8	71	14	US-10-224-836-93	Sequence 93, Appl
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C 327	27	10.8	72	12	US-10-008-524A-174	Sequence 174, App
C 328	27	10.8	72	14	US-10-224-836-94	Sequence 94, Appl
C 329	27	10.8	73	12	US-10-008-524A-178	Sequence 178, App
C 330	27	10.8	73	14	US-10-077-319-1	Sequence 1, Appli
C 331	27	10.8	73	14	US-10-224-836-95	Sequence 95, Appl
C 332	27	10.8	74	14	US-10-224-836-96	Sequence 96, Appl
C 333	27	10.8	75	10	US-09-833-381-884	Sequence 884, App
C 334	27	10.8	75	14	US-10-224-836-97	Sequence 97, Appl
C 335	27	10.8	76	11	US-09-860-474-57	Sequence 57, Appl
C 336	27	10.8	76	12	US-10-409-565-57	Sequence 57, Appl
C 337	27	10.8	76	14	US-10-224-836-98	Sequence 98, Appl
C 338	27	10.8	77	11	US-09-860-474-1	Sequence 1, Appli
C 339	27	10.8	77	11	US-09-916-443A-4	Sequence 4, Appli
C 340	27	10.8	77	12	US-10-037-986-38	Sequence 38, Appl
C 341	27	10.8	77	12	US-10-409-565-1	Sequence 1, Appli
C 342	27	10.8	77	12	US-09-974-330-1	Sequence 1, Appli
C 343	27	10.8	77	12	US-10-408-085-38	Sequence 38, Appl
C 344	27	10.8	77	14	US-10-224-836-99	Sequence 99, Appl
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C 346	27	10.8	78	9	US-09-908-131-1	Sequence 1, Appli
C 347	27	10.8	78	10	US-09-907-795-1	Sequence 1, Appli
C 348	27	10.8	78	14	US-10-124-884-1	Sequence 1, Appli
C 349	27	10.8	78	14	US-10-224-836-100	Sequence 100, App
C 350	27	10.8	79	14	US-10-224-836-101	Sequence 101, App
C 351	27	10.8	80	14	US-10-224-836-102	Sequence 102, App
C 352	27	10.8	81	14	US-10-224-836-103	Sequence 103, App
C 353	27	10.8	82	13	US-10-087-171-6	Sequence 6, Appli
C 354	27	10.8	82	14	US-10-224-836-104	Sequence 104, App
C 355	27	10.8	83	14	US-10-224-836-105	Sequence 105, App
C 356	27	10.8	84	14	US-10-224-836-106	Sequence 106, App
C 357	27	10.8	85	14	US-10-224-836-107	Sequence 107, App
C 358	27	10.8	86	10	US-09-781-902-63	Sequence 63, Appl
C 359	27	10.8	86	14	US-10-224-836-108	Sequence 108, App
C 360	27	10.8	87	11	US-09-916-443A-2	Sequence 2, Appli
C 361	27	10.8	87	12	US-10-223-666-49	Sequence 49, Appl
C 362	27	10.8	87	12	US-10-223-666-52	Sequence 52, Appl
C 363	27	10.8	87	13	US-10-096-830-44	Sequence 44, Appl
C 364	27	10.8	87	14	US-10-224-836-109	Sequence 109, App
C 365	27	10.8	88	14	US-10-224-836-110	Sequence 110, App
C 366	27	10.8	89	14	US-10-224-836-111	Sequence 111, App
C 367	27	10.8	90	10	US-09-780-929-100	Sequence 100, App
C 368	27	10.8	90	12	US-10-008-524A-177	Sequence 177, App
C 369	27	10.8	90	14	US-10-224-836-112	Sequence 112, App
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C 371	27	10.8	92	14	US-10-224-836-114	Sequence 114, App
C 372	27	10.8	93	14	US-10-224-836-115	Sequence 115, App
C 373	27	10.8	94	14	US-10-224-836-116	Sequence 116, App
C 374	27	10.8	95	14	US-10-224-836-117	Sequence 117, App
C 375	27	10.8	96	11	US-09-851-486-36	Sequence 36, Appl
C 376	27	10.8	96	12	US-10-223-666-125	Sequence 125, App
C 377	27	10.8	96	14	US-10-224-836-118	Sequence 118, App
C 378	27	10.8	97	10	US-09-780-929-102	Sequence 102, App
C 379	27	10.8	97	11	US-09-849-928-248	Sequence 248, App
C 380	27	10.8	97	11	US-09-849-928-390	Sequence 390, App
C 381	27	10.8	97	14	US-10-066-960-248	Sequence 248, App

C 382	27	10.8	97	14	US-10-066-960-390	Sequence 390, App	455	27	10.8	431	12	US-10-027-632-253666	Sequence 253666,
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C 384	27	10.8	98	14	US-10-224-836-120	Sequence 120, App	C 457	27	10.8	434	11	US-09-910-082A-117	Sequence 117, App
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C 386	27	10.8	100	14	US-10-224-836-122	Sequence 122, App	459	27	10.8	436	12	US-09-814-353-11340	Sequence 11340, A
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C 389	27	10.8	103	11	US-09-952-680A-4	Sequence 4, Appli	C 462	27	10.8	451	11	US-09-918-995-24108	Sequence 24108, A
C 390	27	10.8	103	14	US-10-224-836-125	Sequence 125, App	C 463	27	10.8	455	11	US-09-918-995-15038	Sequence 15038, A
C 391	27	10.8	104	13	US-10-024-997-1	Sequence 1, Appli	464	27	10.8	455	12	US-09-814-353-5293	Sequence 5293, App
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C 393	27	10.8	105	14	US-10-224-836-127	Sequence 127, App	C 466	27	10.8	462	11	US-09-918-995-14241	Sequence 14241, A
C 394	27	10.8	106	14	US-10-224-836-128	Sequence 128, App	C 467	27	10.8	462	11	US-09-918-995-19257	Sequence 19257, A
C 395	27	10.8	107	14	US-10-224-836-129	Sequence 129, App	C 468	27	10.8	467	12	US-10-082-828A-138	Sequence 138, App
C 396	27	10.8	108	14	US-10-224-836-130	Sequence 130, App	C 469	27	10.8	470	12	US-10-027-632-260668	Sequence 260668,
C 397	27	10.8	109	14	US-10-224-836-131	Sequence 131, App	C 470	27	10.8	470	12	US-10-027-632-260669	Sequence 260669,
C 398	27	10.8	110	9	US-09-815-171A-14	Sequence 14, Appl	C 471	27	10.8	470	13	US-10-027-632-260668	Sequence 260668,
C 399	27	10.8	110	9	US-09-815-171A-14	Sequence 14, Appl	C 472	27	10.8	470	13	US-10-027-632-260669	Sequence 260669,
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C 401	27	10.8	111	14	US-10-224-836-133	Sequence 133, App	C 474	27	10.8	474	11	US-09-918-995-11062	Sequence 11062, A
C 402	27	10.8	112	14	US-10-224-836-134	Sequence 134, App	C 475	27	10.8	477	11	US-09-918-995-20420	Sequence 20420, A
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C 404	27	10.8	114	14	US-10-224-836-136	Sequence 136, App	C 477	27	10.8	478	13	US-10-027-632-270575	Sequence 270575,
C 405	27	10.8	116	11	US-09-883-119A-7	Sequence 7, Appli	C 478	27	10.8	481	11	US-09-918-995-20978	Sequence 20978, A
C 406	27	10.8	123	10	US-09-781-902-55	Sequence 55, Appl	479	27	10.8	484	11	US-09-918-995-23299	Sequence 23299, A
C 407	27	10.8	147	11	US-09-916-443A-6	Sequence 6, Appli	480	27	10.8	486	11	US-09-918-995-23155	Sequence 23155, A
C 408	27	10.8	147	11	US-09-916-443A-7	Sequence 7, Appli	C 481	27	10.8	486	11	US-09-918-995-23155	Sequence 23155, A
C 409	27	10.8	147	11	US-09-916-443A-7	Sequence 7, Appli	C 482	27	10.8	486	12	US-09-814-353-1784	Sequence 1784, App
C 410	27	10.8	154	10	US-09-884-566-7	Sequence 7, Appli	C 483	27	10.8	486	12	US-09-814-353-5206	Sequence 5206, App
C 411	27	10.8	159	9	US-09-923-876-6037	Sequence 6037, App	C 484	27	10.8	486	12	US-09-814-353-8132	Sequence 8132, App
C 412	27	10.8	224	9	US-09-923-876-1319	Sequence 1319, App	485	27	10.8	486	12	US-09-814-353-11493	Sequence 11493, App
C 413	27	10.8	233	9	US-09-294-093B-5344	Sequence 5344, App	486	27	10.8	486	14	US-10-198-846-14035	Sequence 14035, A
C 414	27	10.8	245	9	US-09-923-876-2542	Sequence 2542, App	487	27	10.8	487	14	US-10-034-934-30	Sequence 30, Appl
C 415	27	10.8	247	9	US-09-294-093B-1205	Sequence 1205, App	488	27	10.8	488	11	US-09-918-995-1622	Sequence 1622, App
C 416	27	10.8	256	9	US-09-923-876-388	Sequence 388, App	C 489	27	10.8	488	11	US-09-918-995-15307	Sequence 15307, A
C 417	27	10.8	258	9	US-09-923-876-583	Sequence 583, App	C 490	27	10.8	488	11	US-09-918-995-20849	Sequence 20849, A
C 418	27	10.8	258	9	US-09-923-876-583	Sequence 583, App	C 491	27	10.8	488	11	US-09-918-995-22476	Sequence 22476, A
C 419	27	10.8	263	9	US-09-923-876-2037	Sequence 2037, App	C 492	27	10.8	490	11	US-09-918-995-23760	Sequence 23760, A
C 420	27	10.8	269	9	US-09-923-876-160	Sequence 160, App	C 493	27	10.8	490	11	US-09-918-995-24758	Sequence 24758, A
C 421	27	10.8	272	9	US-09-923-876-5522	Sequence 5522, App	C 494	27	10.8	492	14	US-10-198-846-10882	Sequence 10882, A
C 422	27	10.8	278	12	US-10-027-632-177885	Sequence 177885,	C 495	27	10.8	493	10	US-09-736-457-13	Sequence 13, Appl
C 423	27	10.8	278	13	US-10-027-632-177885	Sequence 177885,	496	27	10.8	493	10	US-09-902-941-13	Sequence 13, Appl
C 424	27	10.8	282	9	US-09-294-093B-3390	Sequence 3390, App	C 497	27	10.8	493	10	US-09-849-626-13	Sequence 13, Appl
C 425	27	10.8	282	13	US-10-016-634A-30	Sequence 30, Appl	C 498	27	10.8	493	11	US-09-918-995-20998	Sequence 20998, A
C 426	27	10.8	283	9	US-09-923-876-5486	Sequence 5486, App	C 499	27	10.8	493	11	US-09-476-300-13	Sequence 13, Appl
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C 428	27	10.8	290	9	US-09-294-093B-399	Sequence 399, App	C 501	27	10.8	493	14	US-10-017-754-13	Sequence 13, Appl
C 429	27	10.8	301	10	US-09-833-381-1013	Sequence 1013, App	C 502	27	10.8	495	11	US-09-918-995-27206	Sequence 27206, A
C 430	27	10.8	311	10	US-09-833-381-1014	Sequence 1014, App	C 503	27	10.8	495	12	US-09-814-353-5212	Sequence 5212, App
C 431	27	10.8	327	14	US-10-198-846-10739	Sequence 10739, A	C 504	27	10.8	495	12	US-09-814-353-11499	Sequence 11499, A
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C 436	27	10.8	345	12	US-09-814-353-854	Sequence 854, App	C 509	27	10.8	506	11	US-09-918-995-12167	Sequence 12167, A
C 437	27	10.8	345	12	US-10-040-997-16	Sequence 16, Appl	C 510	27	10.8	506	11	US-09-918-995-19851	Sequence 19851, A
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C 439	27	10.8	352	12	US-09-814-353-21234	Sequence 21234, A	C 512	27	10.8	509	11	US-09-918-995-24565	Sequence 24565, A
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C 441	27	10.8	364	10	US-09-747-835A-17	Sequence 17, Appl	C 514	27	10.8	512	12	US-09-814-353-5072	Sequence 5072, App
C 442	27	10.8	365	12	US-09-814-353-19505	Sequence 19505, A	C 515	27	10.8	512	12	US-09-814-353-11364	Sequence 11364, A
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C 444	27	10.8	373	12	US-10-027-632-256783	Sequence 256783,	C 517	27	10.8	517	12	US-09-814-353-1134	Sequence 1134, App
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C 447	27	10.8	382	14	US-10-198-846-11789	Sequence 11789, A	C 520	27	10.8	521	13	US-10-027-632-265935	Sequence 265935,
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C 450	27	10.8	416	11	US-09-918-995-14235	Sequence 14235, A	C 523	27	10.8	530	14	US-10-198-846-12683	Sequence 12683, A
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C 454	27	10.8	429	12	US-09-814-353-20728	Sequence 20728, A	527	27	10.8	544	10	US-09-757-781-45	Sequence 45, Appl



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C 529	27	10.8	550	12	US-09-814-353-19825	Sequence 19825, A	602	27	10.8	631	14	US-10-198-846-8336	Sequence 8336, Ap
C 530	27	10.8	551	11	US-09-918-995-26125	Sequence 26125, A	603	27	10.8	636	12	US-10-027-632-281852	Sequence 281852,
C 531	27	10.8	555	11	US-09-918-995-13190	Sequence 13190, A	C 604	27	10.8	636	12	US-10-027-632-281852	Sequence 281852,
C 532	27	10.8	557	11	US-09-918-995-29207	Sequence 29207, A	605	27	10.8	636	13	US-10-027-632-281852	Sequence 281852,
C 533	27	10.8	559	12	US-09-814-353-2617	Sequence 2617, Ap	C 606	27	10.8	636	13	US-10-027-632-281852	Sequence 281852,
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C 543	27	10.8	564	11	US-09-918-995-16187	Sequence 16187, A	616	27	10.8	655	14	US-10-198-846-9659	Sequence 9659, Ap
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C 546	27	10.8	570	14	US-10-158-646-8	Sequence 8, Appli	C 619	27	10.8	664	14	US-10-198-846-8060	Sequence 8060, Ap
C 547	27	10.8	572	12	US-10-027-632-184982	Sequence 184982,	C 620	27	10.8	664	14	US-10-198-846-8060	Sequence 8060, Ap
C 548	27	10.8	572	13	US-10-027-632-184982	Sequence 184982,	C 621	27	10.8	665	14	US-10-198-846-1717	Sequence 1717, Ap
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C 551	27	10.8	575	11	US-09-918-995-10295	Sequence 10295, A	C 624	27	10.8	687	9	US-09-962-436-41	Sequence 41, Appl
C 552	27	10.8	576	12	US-09-814-353-5862	Sequence 5862, Ap	C 625	27	10.8	687	12	US-09-873-319-652	Sequence 652, App
C 553	27	10.8	576	12	US-09-814-353-12143	Sequence 12143, A	C 626	27	10.8	687	12	US-09-960-706-996	Sequence 996, App
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C 557	27	10.8	580	11	US-09-918-995-13250	Sequence 13250, A	630	27	10.8	689	13	US-10-027-632-231169	Sequence 231169,
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C 560	27	10.8	585	12	US-10-027-632-187960	Sequence 187960,	C 633	27	10.8	702	14	US-10-198-846-2127	Sequence 2127, Ap
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C 563	27	10.8	594	9	US-09-812-102-77	Sequence 77, Appl	C 636	27	10.8	717	12	US-10-027-632-278291	Sequence 278291,
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C 568	27	10.8	598	12	US-10-027-632-232149	Sequence 232149,	C 641	27	10.8	717	13	US-10-027-632-278293	Sequence 278293,
C 569	27	10.8	598	12	US-10-027-632-232150	Sequence 232150,	C 642	27	10.8	726	14	US-10-198-846-10726	Sequence 10726, A
C 570	27	10.8	598	12	US-10-027-632-232151	Sequence 232151,	643	27	10.8	727	13	US-10-001-879-84	Sequence 84, Appl
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C 574	27	10.8	598	13	US-10-027-632-232150	Sequence 232150,	C 647	27	10.8	734	10	US-09-995-494-13	Sequence 13, Appl
C 575	27	10.8	598	13	US-10-027-632-232151	Sequence 232151,	C 648	27	10.8	742	9	US-09-910-943-352	Sequence 352, App
C 576	27	10.8	600	14	US-10-198-846-9355	Sequence 9355, Ap	649	27	10.8	742	12	US-10-027-632-253983	Sequence 253983,
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582	27	10.8	602	14	US-10-040-862-7277	Sequence 7277, Ap	C 655	27	10.8	762	14	US-10-082-830-133	Sequence 133, App
583	27	10.8	604	12	US-09-814-353-19787	Sequence 19787, A	C 656	27	10.8	772	12	US-09-814-353-4407	Sequence 4407, Ap
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C 599	27	10.8	623	13	US-10-027-632-250371	Sequence 250371,	C 672	27	10.8	801	13	US-10-027-632-258008	Sequence 258008,
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691	27	10.8	832	12	US-10-027-632-250911	Sequence 250911, Ap	764	27	10.8	982	12	US-10-017-161-1923	Sequence 1923, Ap
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704	27	10.8	850	12	US-09-814-353-20285	Sequence 20285, A	c 777	27	10.8	1007	13	US-10-202-193-106	Sequence 106, App
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708	27	10.8	856	12	US-10-017-161-1447	Sequence 1447, App	781	27	10.8	1020	12	US-10-082-828A-36	Sequence 36, Appl
709	27	10.8	857	12	US-10-006-285-292	Sequence 292, App	c 782	27	10.8	1020	12	US-10-082-828A-36	Sequence 36, Appl
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711	27	10.8	858	14	US-10-198-846-3300	Sequence 3300, Ap	784	27	10.8	1024	12	US-10-027-632-252437	Sequence 252437, Ap
712	27	10.8	858	14	US-10-198-846-13318	Sequence 13318, A	c 785	27	10.8	1024	13	US-10-202-193-44	Sequence 44, Appl
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714	27	10.8	861	14	US-10-198-846-3064	Sequence 3064, Ap	c 787	27	10.8	1024	13	US-10-202-193-49	Sequence 49, Appl
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725	27	10.8	884	12	US-10-027-632-261815	Sequence 261815, Ap	798	27	10.8	1061	13	US-10-011-445-40	Sequence 40, Appl
726	27	10.8	884	12	US-10-027-632-261816	Sequence 261816, Ap	799	27	10.8	1063	12	US-10-017-161-1005	Sequence 1005, Ap
727	27	10.8	884	13	US-10-027-632-261814	Sequence 261814, Ap	800	27	10.8	1069	12	US-10-017-161-991	Sequence 991, App
728	27	10.8	884	13	US-10-027-632-261815	Sequence 261815, Ap	c 801	27	10.8	1069	12	US-10-017-161-1415	Sequence 1415, Ap
729	27	10.8	884	13	US-10-027-632-261816	Sequence 261816, Ap	802	27	10.8	1073	14	US-10-198-846-6810	Sequence 6810, Ap
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733	27	10.8	898	12	US-09-814-353-19884	Sequence 19884, A	c 806	27	10.8	1089	10	US-09-880-107-2087	Sequence 2087, Ap
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736	27	10.8	904	12	US-10-027-632-251511	Sequence 251511, Ap	809	27	10.8	1091	12	US-09-814-353-19819	Sequence 19819, A
737	27	10.8	904	12	US-10-027-632-251512	Sequence 251512, Ap	810	27	10.8	1096	12	US-10-017-161-2315	Sequence 2315, Ap
738	27	10.8	904	13	US-10-027-632-251510	Sequence 251510, Ap	c 811	27	10.8	1099	12	US-10-027-632-255168	Sequence 255168, Ap
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741	27	10.8	909	14	US-10-198-846-2884	Sequence 2884, Ap	814	27	10.8	1100	12	US-10-027-632-257049	Sequence 257049, Ap
742	27	10.8	910	12	US-10-017-161-1425	Sequence 1425, Ap	815	27	10.8	1100	13	US-10-027-632-257048	Sequence 257048, Ap
743	27	10.8	910	14	US-10-198-846-4726	Sequence 4726, Ap	816	27	10.8	1100	13	US-10-027-632-257049	Sequence 257049, Ap
744	27	10.8	910	14	US-10-198-846-5574	Sequence 5574, Ap	817	27	10.8	1102	12	US-10-027-632-257049	Sequence 257049, Ap
745	27	10.8	914	14	US-10-198-846-9029	Sequence 9029, Ap	c 818	27	10.8	1107	12	US-10-017-161-287	Sequence 287, App
746	27	10.8	917	14	US-10-198-846-7095	Sequence 7095, Ap	c 819	27	10.8	1108	12	US-10-241-220-52	Sequence 52, Appli
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C 820	27	10.8	1109	9	US-09-349-015-19	Sequence 19, Appl	C 893	27	10.8	1302	14	US-10-245-880-69	Sequence 69, Appl
C 821	27	10.8	1109	15	US-10-219-664-15	Sequence 15, Appl	C 894	27	10.8	1302	14	US-10-245-033-69	Sequence 69, Appl
C 822	27	10.8	1118	14	US-10-198-846-5504	Sequence 5504, Ap	C 895	27	10.8	1302	14	US-10-243-095-69	Sequence 69, Appl
C 823	27	10.8	1143	12	US-09-814-353-21392	Sequence 21392, A	C 896	27	10.8	1302	14	US-10-245-185-69	Sequence 69, Appl
C 824	27	10.8	1146	14	US-10-177-900-9	Sequence 9, Appll	C 897	27	10.8	1302	14	US-10-245-427-69	Sequence 69, Appl
C 825	27	10.8	1155	10	US-09-833-381-1293	Sequence 1293, Ap	C 898	27	10.8	1302	14	US-10-245-473-69	Sequence 69, Appl
C 826	27	10.8	1159	12	US-10-017-161-2319	Sequence 2319, Ap	C 899	27	10.8	1302	14	US-10-245-770-69	Sequence 69, Appl
827	27	10.8	1166	12	US-10-241-220-5	Sequence 5, Appli	C 900	27	10.8	1302	14	US-10-245-877-69	Sequence 69, Appl
828	27	10.8	1173	12	US-10-082-828A-89	Sequence 89, Appl	C 901	27	10.8	1302	14	US-10-246-976-69	Sequence 69, Appl
829	27	10.8	1177	12	US-10-017-161-1439	Sequence 1439, Ap	C 902	27	10.8	1302	14	US-10-243-320-69	Sequence 69, Appl
C 830	27	10.8	1180	12	US-10-017-161-2209	Sequence 2209, Ap	C 903	27	10.8	1302	14	US-10-242-743-69	Sequence 69, Appl
C 831	27	10.8	1192	12	US-10-017-161-511	Sequence 511, App	C 904	27	10.8	1302	14	US-10-242-845-69	Sequence 69, Appl
832	27	10.8	1192	12	US-10-017-161-1273	Sequence 1273, Ap	C 905	27	10.8	1302	14	US-10-237-636-69	Sequence 69, Appl
C 833	27	10.8	1195	12	US-10-017-161-993	Sequence 993, App	C 906	27	10.8	1302	14	US-10-238-325-69	Sequence 69, Appl
834	27	10.8	1198	12	US-10-252-157-371	Sequence 371, App	C 907	27	10.8	1302	14	US-10-238-346-69	Sequence 69, Appl
C 835	27	10.8	1198	14	US-10-011-585A-98	Sequence 98, Appl	C 908	27	10.8	1302	14	US-10-238-411-69	Sequence 69, Appl
C 836	27	10.8	1202	12	US-09-814-353-20311	Sequence 20311, A	C 909	27	10.8	1302	14	US-10-243-124-69	Sequence 69, Appl
837	27	10.8	1202	12	US-10-027-632-265472	Sequence 265472,	C 910	27	10.8	1302	14	US-10-243-425-69	Sequence 69, Appl
838	27	10.8	1202	13	US-10-027-632-265472	Sequence 265472,	C 911	27	10.8	1302	14	US-10-243-446-69	Sequence 69, Appl
839	27	10.8	1203	12	US-09-971-392-218	Sequence 218, App	C 912	27	10.8	1302	14	US-10-245-874-69	Sequence 69, Appl
840	27	10.8	1206	12	US-10-027-632-253044	Sequence 253044,	C 913	27	10.8	1302	14	US-10-242-653-69	Sequence 69, Appl
841	27	10.8	1206	12	US-10-027-632-253045	Sequence 253045,	C 914	27	10.8	1302	14	US-10-243-167-69	Sequence 69, Appl
842	27	10.8	1206	13	US-10-027-632-253044	Sequence 253044,	C 915	27	10.8	1302	14	US-10-243-388-69	Sequence 69, Appl
843	27	10.8	1206	13	US-10-027-632-253045	Sequence 253045,	C 916	27	10.8	1302	14	US-10-244-947-69	Sequence 69, Appl
844	27	10.8	1214	10	US-09-833-381-1595	Sequence 1595, Ap	C 917	27	10.8	1302	14	US-10-244-968-69	Sequence 69, Appl
845	27	10.8	1225	12	US-10-017-161-2083	Sequence 2083, Ap	C 918	27	10.8	1302	14	US-10-244-990-69	Sequence 69, Appl
846	27	10.8	1230	12	US-10-027-632-254828	Sequence 254828,	C 919	27	10.8	1302	14	US-10-245-079-69	Sequence 69, Appl
847	27	10.8	1230	13	US-10-027-632-254828	Sequence 254828,	C 920	27	10.8	1302	14	US-10-245-127-69	Sequence 69, Appl
848	27	10.8	1231	12	US-10-017-161-2267	Sequence 2267, Ap	C 921	27	10.8	1302	14	US-10-245-207-69	Sequence 69, Appl
C 849	27	10.8	1243	12	US-10-027-632-251629	Sequence 251629,	C 922	27	10.8	1302	14	US-10-245-646-69	Sequence 69, Appl
C 850	27	10.8	1243	13	US-10-027-632-251629	Sequence 251629,	C 923	27	10.8	1302	14	US-10-245-695-69	Sequence 69, Appl
C 851	27	10.8	1259	12	US-09-971-392-199	Sequence 199, App	C 924	27	10.8	1302	14	US-10-245-699-69	Sequence 69, Appl
852	27	10.8	1267	12	US-10-017-161-1405	Sequence 1405, Ap	C 925	27	10.8	1302	14	US-10-245-737-69	Sequence 69, Appl
C 853	27	10.8	1279	12	US-10-017-161-523	Sequence 523, App	C 926	27	10.8	1302	14	US-10-245-878-69	Sequence 69, Appl
854	27	10.8	1282	12	US-10-017-161-999	Sequence 999, App	C 927	27	10.8	1302	14	US-10-245-890-69	Sequence 69, Appl
855	27	10.8	1285	12	US-10-017-161-2163	Sequence 2163, Ap	C 928	27	10.8	1302	14	US-10-245-899-69	Sequence 69, Appl
C 856	27	10.8	1285	12	US-10-017-161-2317	Sequence 2317, Ap	C 929	27	10.8	1302	14	US-10-245-900-69	Sequence 69, Appl
C 857	27	10.8	1294	14	US-10-198-846-10457	Sequence 10457, A	C 930	27	10.8	1302	14	US-10-247-058-69	Sequence 69, Appl
858	27	10.8	1296	12	US-10-027-632-257449	Sequence 257449,	C 931	27	10.8	1302	14	US-10-245-454-69	Sequence 69, Appl
859	27	10.8	1296	13	US-10-027-632-257449	Sequence 257449,	C 932	27	10.8	1302	14	US-10-237-471-69	Sequence 69, Appl
C 860	27	10.8	1297	12	US-10-017-161-2295	Sequence 2295, Ap	C 933	27	10.8	1302	14	US-10-238-261-69	Sequence 69, Appl
C 861	27	10.8	1302	12	US-10-237-496-69	Sequence 69, Appl	C 934	27	10.8	1302	14	US-10-238-324-69	Sequence 69, Appl
C 862	27	10.8	1302	12	US-10-242-074-69	Sequence 69, Appl	C 935	27	10.8	1302	14	US-10-241-860-69	Sequence 69, Appl
C 863	27	10.8	1302	12	US-10-242-505-69	Sequence 69, Appl	C 936	27	10.8	1302	14	US-10-242-172-69	Sequence 69, Appl
C 864	27	10.8	1302	12	US-10-242-574-69	Sequence 69, Appl	C 937	27	10.8	1302	14	US-10-242-652-69	Sequence 69, Appl
C 865	27	10.8	1302	12	US-10-243-261-69	Sequence 69, Appl	C 938	27	10.8	1302	14	US-10-242-990-69	Sequence 69, Appl
C 866	27	10.8	1302	12	US-10-243-282-69	Sequence 69, Appl	C 939	27	10.8	1302	14	US-10-243-023-69	Sequence 69, Appl
C 867	27	10.8	1302	12	US-10-243-402-69	Sequence 69, Appl	C 940	27	10.8	1302	14	US-10-243-103-69	Sequence 69, Appl
C 868	27	10.8	1302	12	US-10-243-431-69	Sequence 69, Appl	C 941	27	10.8	1302	14	US-10-243-276-69	Sequence 69, Appl
C 869	27	10.8	1302	12	US-10-245-164-69	Sequence 69, Appl	C 942	27	10.8	1302	14	US-10-243-326-69	Sequence 69, Appl
C 870	27	10.8	1302	12	US-10-244-972-69	Sequence 69, Appl	C 943	27	10.8	1302	14	US-10-243-364-69	Sequence 69, Appl
C 871	27	10.8	1302	12	US-10-197-942-69	Sequence 69, Appl	C 944	27	10.8	1302	14	US-10-243-494-69	Sequence 69, Appl
C 872	27	10.8	1302	12	US-10-238-196-69	Sequence 69, Appl	C 945	27	10.8	1302	14	US-10-244-995-69	Sequence 69, Appl
C 873	27	10.8	1302	12	US-10-245-013-69	Sequence 69, Appl	C 946	27	10.8	1302	14	US-10-245-230-69	Sequence 69, Appl
C 874	27	10.8	1302	14	US-10-245-103-69	Sequence 69, Appl	C 947	27	10.8	1302	14	US-10-245-253-69	Sequence 69, Appl
C 875	27	10.8	1302	14	US-10-245-107-69	Sequence 69, Appl	C 948	27	10.8	1302	14	US-10-245-479-69	Sequence 69, Appl
C 876	27	10.8	1302	14	US-10-245-143-69	Sequence 69, Appl	C 949	27	10.8	1302	14	US-10-245-499-69	Sequence 69, Appl
C 877	27	10.8	1302	14	US-10-245-771-69	Sequence 69, Appl	C 950	27	10.8	1302	14	US-10-245-772-69	Sequence 69, Appl
C 878	27	10.8	1302	14	US-10-245-851-69	Sequence 69, Appl	C 951	27	10.8	1302	14	US-10-245-811-69	Sequence 69, Appl
C 879	27	10.8	1302	14	US-10-245-883-69	Sequence 69, Appl	C 952	27	10.8	1302	14	US-10-245-812-69	Sequence 69, Appl
C 880	27	10.8	1302	14	US-10-237-535-69	Sequence 69, Appl	C 953	27	10.8	1302	14	US-10-245-852-69	Sequence 69, Appl
C 881	27	10.8	1302	14	US-10-238-183-69	Sequence 69, Appl	C 954	27	10.8	1302	14	US-10-245-875-69	Sequence 69, Appl
C 882	27	10.8	1302	14	US-10-238-283-69	Sequence 69, Appl	C 955	27	10.8	1302	14	US-10-245-881-69	Sequence 69, Appl
C 883	27	10.8	1302	14	US-10-238-370-69	Sequence 69, Appl	C 956	27	10.8	1302	14	US-10-245-911-69	Sequence 69, Appl
C 884	27	10.8	1302	14	US-10-245-055-69	Sequence 69, Appl	C 957	27	10.8	1302	14	US-10-245-913-69	Sequence 69, Appl
C 885	27	10.8	1302	14	US-10-245-147-69	Sequence 69, Appl	C 958	27	10.8	1302	14	US-10-246-080-69	Sequence 69, Appl
C 886	27	10.8	1302	14	US-10-245-730-69	Sequence 69, Appl	C 959	27	10.8	1302	14	US-10-246-121-69	Sequence 69, Appl
C 887	27	10.8	1302	14	US-10-245-739-69	Sequence 69, Appl	C 960	27	10.8	1302	14	US-10-246-305-69	Sequence 69, Appl
C 888	27	10.8	1302	14	US-10-246-210-69	Sequence 69, Appl	C 961	27	10.8	1302	14	US-10-246-929-69	Sequence 69, Appl
C 889	27	10.8	1302	14	US-10-239-196-69	Sequence 69, Appl	C 962	27	10.8	1302	14	US-10-247-036-69	Sequence 69, Appl
C 890	27	10.8	1302	14	US-10-243-024-69	Sequence 69, Appl	C 963	27	10.8	1302	14	US-10-243-255-69	Sequence 69, Appl
C 891	27	10.8	1302	14	US-10-243-409-69	Sequence 69, Appl	C 964	27	10.8	1302	14	US-10-245-810-69	Sequence 69, Appl
C 892	27	10.8	1302	14	US-10-245-621-69	Sequence 69, Appl	C 965	27	10.8	1302	14	US-10-245-910-69	Sequence 69, Appl

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c 966      27 10.8 1302 14 US-10-246-098-69 Sequence 69, Appl
c 967      27 10.8 1310 14 US-10-198-846-12930 Sequence 12930, A
c 968      27 10.8 1311 12 US-09-814-353-19812 Sequence 19812, A
c 969      27 10.8 1324 12 US-10-017-161-2297 Sequence 2297, Ap
c 970      27 10.8 1333 12 US-10-017-161-1921 Sequence 1921, Ap
c 971      27 10.8 1333 12 US-10-017-161-2111 Sequence 2111, Ap
c 972      27 10.8 1334 12 US-10-027-632-265790 Sequence 265790,
c 973      27 10.8 1334 12 US-10-027-632-265791 Sequence 265791,
c 974      27 10.8 1334 13 US-10-027-632-265790 Sequence 265790,
c 975      27 10.8 1334 13 US-10-027-632-265791 Sequence 265791,
c 976      27 10.8 1345 12 US-10-017-161-1443 Sequence 1443, Ap
c 977      27 10.8 1348 12 US-10-017-161-2075 Sequence 2075, Ap
c 978      27 10.8 1372 12 US-10-017-161-2277 Sequence 2277, Ap
c 979      27 10.8 1375 14 US-10-176-847-33 Sequence 33, Appl
c 980      27 10.8 1376 12 US-09-971-392-155 Sequence 155, App
c 981      27 10.8 1376 12 US-09-971-392-155 Sequence 155, App
c 982      27 10.8 1387 12 US-10-017-161-2269 Sequence 2269, Ap
c 983      27 10.8 1390 12 US-10-017-161-945 Sequence 945, App
c 984      27 10.8 1395 12 US-09-814-353-21813 Sequence 21813, A
c 985      27 10.8 1396 12 US-10-017-161-2373 Sequence 2373, Ap
c 986      27 10.8 1406 14 US-10-198-846-10016 Sequence 10016, A
c 987      27 10.8 1411 12 US-10-017-161-2279 Sequence 2279, Ap
c 988      27 10.8 1414 12 US-10-017-161-531 Sequence 531, App
c 989      27 10.8 1417 12 US-10-017-161-2139 Sequence 2139, Ap
c 990      27 10.8 1427 14 US-10-198-846-13745 Sequence 13745, A
c 991      27 10.8 1432 14 US-10-198-846-10035 Sequence 10035, A
c 992      27 10.8 1433 14 US-10-198-846-4247 Sequence 4247, Ap
c 993      27 10.8 1435 12 US-10-017-161-1953 Sequence 1953, Ap
c 994      27 10.8 1438 12 US-10-017-161-541 Sequence 541, App
c 995      27 10.8 1440 12 US-10-176-464A-66 Sequence 66, Appl
c 996      27 10.8 1453 9 US-09-349-015-14 Sequence 14, Appl
c 997      27 10.8 1453 14 US-10-198-846-13730 Sequence 13730, A
c 998      27 10.8 1453 15 US-10-219-664-10 Sequence 10, Appl
c 999      27 10.8 1455 12 US-10-252-157-389 Sequence 389, App
c1000     27 10.8 1457 12 US-09-814-353-21594 Sequence 21594, A
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ALIGNMENTS

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RESULT 1
JS-09-978-167-3
Sequence 3, Application US/09978167
Publication No. US2003007775A1
GENERAL INFORMATION:
APPLICANT: YAN, Chunhua et al.
TITLE OF INVENTION: ISOLATED HUMAN SECRETED PROTEINS,
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN SECRETED PROTEINS, AND
TITLE OF INVENTION: USES THEREOF
FILE REFERENCE: CL001303
CURRENT APPLICATION NUMBER: US/09/978,167
CURRENT FILING DATE: 2001-10-17
NUMBER OF SEQ ID NOS: 6
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 3
LENGTH: 78785
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
LOCATION: (1)..(78785)
OTHER INFORMATION: n = A,T,C or G
JS-09-978-167-3
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Query Match 13.1%; Score 33; DB 11; Length 78785;
Best Local Similarity 100.0%; Pred. No. 6.4e-08;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Y 92 AAAAAATC-----NNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 124
|||||
b 69776 AAAAAATC-----NNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 69808
|||||
```

```
RESULT 2
US-10-155-693-21/c
Sequence 21, Application US/10155693
Publication No. US20030175876A1
GENERAL INFORMATION:
APPLICANT: FOX, GARY M.
APPLICANT: JING, SHUQIAN
APPLICANT: WEN, DUANZHI
TITLE OF INVENTION: GLIAL CELL LINE-DERIVED NEUROTROPHIC FACTOR RECEPTOR
FILE REFERENCE: A-401C
CURRENT APPLICATION NUMBER: US/10/155,693
CURRENT FILING DATE: 2002-05-24
PRIOR APPLICATION NUMBER: US/08/837,199
PRIOR FILING DATE: 1997-04-14
PRIOR APPLICATION NUMBER: US 60/015,907
PRIOR FILING DATE: 1996-04-22
PRIOR APPLICATION NUMBER: US 60/017,221
NUMBER OF SEQ ID NOS: 47
SOFTWARE: PatentIn version 3.1
SEQ ID NO 21
LENGTH: 1075
TYPE: DNA
ORGANISM: HUMAN
FEATURE:
NAME/KEY: CDS
LOCATION: (2)..(445)
OTHER INFORMATION:
FEATURE:
NAME/KEY: misc feature
LOCATION: (1)..(1075)
OTHER INFORMATION: No. US20030175876A1= "1 to 1075 is 1255 to 2330 of Figure 5 He
FEATURE:
NAME/KEY: misc feature
LOCATION: (763)..(801)
OTHER INFORMATION: N in position 763 to 801 indicates positions of divergence betw
OTHER INFORMATION: n different receptor clones.
US-10-155-693-21
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```
Query Match 12.4%; Score 31; DB 12; Length 1075;
Best Local Similarity 100.0%; Pred. No. 6.8e-07;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 94 AAAATC-----NNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 124
|||||
Db 807 AAAATC-----NNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 777
|||||
```

```
RESULT 3
US-10-155-693-46/c
Sequence 46, Application US/10155693
Publication No. US20030175876A1
GENERAL INFORMATION:
APPLICANT: FOX, GARY M.
APPLICANT: JING, SHUQIAN
APPLICANT: WEN, DUANZHI
TITLE OF INVENTION: GLIAL CELL LINE-DERIVED NEUROTROPHIC FACTOR RECEPTOR
FILE REFERENCE: A-401C
CURRENT APPLICATION NUMBER: US/10/155,693
CURRENT FILING DATE: 2002-05-24
PRIOR APPLICATION NUMBER: US/08/837,199
PRIOR FILING DATE: 1997-04-14
PRIOR APPLICATION NUMBER: US 60/015,907
PRIOR FILING DATE: 1996-04-22
PRIOR APPLICATION NUMBER: US 60/017,221
NUMBER OF SEQ ID NOS: 47
SOFTWARE: PatentIn version 3.1
SEQ ID NO 46
LENGTH: 1076
TYPE: DNA
ORGANISM: HUMAN
FEATURE:
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; NAME/KEY: misc feature  
; LOCATION: (586)..(586)  
; OTHER INFORMATION: N in position 586 indicates a position of divergence between diff  
; OTHER INFORMATION: erent receptor clones.  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (764)..(802)  
; OTHER INFORMATION: N in positions 764 to 802 indicates positions of divergence betw  
; OTHER INFORMATION: een different receptor clones.  
US-10-155-693-46

Query Match 12.4%; Score 31; DB 12; Length 1076;  
Best Local Similarity 100.0%; Pred. No. 6.8e-07;  
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 94 AAAATCNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 124  
|||||  
Db 808 AAAATCNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 778  
|||||

## RESULT 4

JS-10-155-693-15/c

Sequence 15, Application US/10155693

Publication No. US20030175876A1

GENERAL INFORMATION:

APPLICANT: FOX, GARY M.

APPLICANT: JING, SHUQIAN

APPLICANT: WEN, DUANZHI

TITLE OF INVENTION: GLIAL CELL LINE-DERIVED NEUROTROPHIC FACTOR RECEPTOR

FILE REFERENCE: A-401C

CURRENT APPLICATION NUMBER: US/10/155,693

CURRENT FILING DATE: 2002-05-24

PRIOR APPLICATION NUMBER: US/08/837,199

PRIOR FILING DATE: 1997-04-14

PRIOR APPLICATION NUMBER: US 60/015,907

PRIOR FILING DATE: 1996-04-22

PRIOR APPLICATION NUMBER: US 60/017,221

PRIOR FILING DATE: 1996-05-09

NUMBER OF SEQ ID NOS: 47

SOFTWARE: PatentIn version 3.1

SEQ ID NO 15

LENGTH: 2157

TYPE: DNA

ORGANISM: HUMAN

FEATURE:

NAME/KEY: CDS

LOCATION: (2)..(886)

OTHER INFORMATION:

FEATURE:

NAME/KEY: misc feature

LOCATION: (1)..(2157)

OTHER INFORMATION: No. US20030175876A1e= "1 to 2157 is 814 to 2971 of Figure 5 29brd

FEATURE:

NAME/KEY: misc feature

LOCATION: (1204)..(1242)

OTHER INFORMATION: N in positions 1204 to 1242 indicates positions of divergence bet

OTHER INFORMATION: ween different receptor clones.

S-10-155-693-15

Query Match

Best Local Similarity 12.4%; Score 31; DB 12; Length 2157;

Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

ry 94 AAAATCNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 124

|||||

b 1248 AAAATCNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 1218

|||||

## RESULT 5

S-10-155-693-43/c

Sequence 43, Application US/10155693

Publication No. US20030175876A1

GENERAL INFORMATION:

; APPLICANT: FOX, GARY M.  
; APPLICANT: JING, SHUQIAN  
; APPLICANT: WEN, DUANZHI  
; TITLE OF INVENTION: GLIAL CELL LINE-DERIVED NEUROTROPHIC FACTOR RECEPTOR  
; FILE REFERENCE: A-401C  
; CURRENT APPLICATION NUMBER: US/10/155,693  
; CURRENT FILING DATE: 2002-05-24  
; PRIOR APPLICATION NUMBER: US/08/837,199  
; PRIOR FILING DATE: 1997-04-14  
; PRIOR APPLICATION NUMBER: US 60/015,907  
; PRIOR FILING DATE: 1996-04-22  
; PRIOR APPLICATION NUMBER: US 60/017,221  
; PRIOR FILING DATE: 1996-05-09  
; NUMBER OF SEQ ID NOS: 47  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 43

LENGTH: 2158

TYPE: DNA

ORGANISM: HUMAN

FEATURE:

NAME/KEY: misc feature

LOCATION: (1027)..(1027)

; OTHER INFORMATION: N in position 1027 indicates a position of divergence between c  
; OTHER INFORMATION: ferent receptor clones.

FEATURE:

NAME/KEY: misc feature

LOCATION: (1205)..(1243)

; OTHER INFORMATION: N in positions 1205 to 1243 indicates positions of divergence  
; OTHER INFORMATION: tween different receptor clones.

US-10-155-693-43

Query Match

Best Local Similarity 12.4%; Score 31; DB 12; Length 2158;

Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 94 AAAATCNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 124

|||||

Db 1249 AAAATCNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 1219

|||||

## RESULT 6

US-10-155-693-1/c

Sequence 1, Application US/10155693

Publication No. US20030175876A1

GENERAL INFORMATION:

APPLICANT: FOX, GARY M.

APPLICANT: JING, SHUQIAN

APPLICANT: WEN, DUANZHI

TITLE OF INVENTION: GLIAL CELL LINE-DERIVED NEUROTROPHIC FACTOR RECEPTOR

FILE REFERENCE: A-401C

CURRENT APPLICATION NUMBER: US/10/155,693

CURRENT FILING DATE: 2002-05-24

PRIOR APPLICATION NUMBER: US/08/837,199

PRIOR FILING DATE: 1997-04-14

PRIOR APPLICATION NUMBER: US 60/015,907

PRIOR FILING DATE: 1996-04-22

PRIOR APPLICATION NUMBER: US 60/017,221

PRIOR FILING DATE: 1996-05-09

NUMBER OF SEQ ID NOS: 47

SOFTWARE: PatentIn version 3.1

SEQ ID NO 1

LENGTH: 2568

TYPE: DNA

ORGANISM: HUMAN

FEATURE:

NAME/KEY: CDS

LOCATION: (540)..(1934)

OTHER INFORMATION:

FEATURE:

NAME/KEY: misc feature

LOCATION: (2078)..(2078)

; OTHER INFORMATION: N in position 2078 indicates a position of divergence between d  
; OTHER INFORMATION: ferent receptor clones



```

;
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (2107)..(2107)
; OTHER INFORMATION: N in position 2107 indicates a position of divergence between dif
; OTHER INFORMATION: ferent receptor clones
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (2241)..(2241)
; OTHER INFORMATION: N in position 2241 indicates a position of divergence between dif
; OTHER INFORMATION: ferent receptor clones
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (2250)..(2250)
; OTHER INFORMATION: N in position 2250 indicates a position of divergence between dif
; OTHER INFORMATION: ferent receptor clones
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (2256)..(2294)
; OTHER INFORMATION: N in positions 2256 to 2294 indicates positions of divergence be
; OTHER INFORMATION: tween different receptor clones
US-10-155-693-1

Query Match      12.4%; Score 31; DB 12; Length 2568;
Best Local Similarity 100.0%; Pred. No. 7.1e-07;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 94 AAAATCNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 124
|||||
Db 2300 AAAATCNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 2270

RESULT 7
US-10-155-693-5/c
; Sequence 5, Application: US/10155693
; Publication No. US20030175876A1
; GENERAL INFORMATION:
; APPLICANT: FOX, GARY M.
; APPLICANT: JING, SHUQIAN
; APPLICANT: WEN, DUANZHI
; TITLE OF INVENTION: GLIAL CELL LINE-DERIVED NEUROTROPHIC FACTOR RECEPTOR
; FILE REFERENCE: A-401C
; CURRENT APPLICATION NUMBER: US/10/155,693
; CURRENT FILING DATE: 2002-05-24
; PRIOR APPLICATION NUMBER: US/08/837,199
; PRIOR FILING DATE: 1997-04-14
; PRIOR APPLICATION NUMBER: US 60/015,907
; PRIOR FILING DATE: 1996-04-22
; PRIOR APPLICATION NUMBER: US 60/017,221
; PRIOR FILING DATE: 1996-05-09
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 3209
; TYPE: DNA
; ORGANISM: HUMAN
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(510)
; OTHER INFORMATION: note="1 to 510 is -237 to 272 of Fig 5 Hsgr-21bf"
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(539)
; OTHER INFORMATION: note="1 to 539 is -237 to 301 of Fig 5 Gdnfr"
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (2078)..(2078)
; OTHER INFORMATION: N in position 2078 indicates a position of divergence between dif
; OTHER INFORMATION: ferent receptor clones
; FEATURE:

```

```

; NAME/KEY: misc feature
; LOCATION: (2256)..(2294)
; OTHER INFORMATION: N in positions 2256 to 2294 indicates positions of divergence ;
; OTHER INFORMATION: ween different receptor clones
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1091)..(1091)
; OTHER INFORMATION: N in position 1091 indicates any nucleic acid
US-10-155-693-5

Query Match      12.4%; Score 31; DB 12; Length 3209;
Best Local Similarity 100.0%; Pred. No. 7.2e-07;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 94 AAAATCNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 124
|||||
Db 2300 AAAATCNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 2270

RESULT 8
US-10-155-693-37/c
; Sequence 37, Application: US/10155693
; Publication No. US20030175876A1
; GENERAL INFORMATION:
; APPLICANT: FOX, GARY M.
; APPLICANT: JING, SHUQIAN
; APPLICANT: WEN, DUANZHI
; TITLE OF INVENTION: GLIAL CELL LINE-DERIVED NEUROTROPHIC FACTOR RECEPTOR
; FILE REFERENCE: A-401C
; CURRENT APPLICATION NUMBER: US/10/155,693
; CURRENT FILING DATE: 2002-05-24
; PRIOR APPLICATION NUMBER: US/08/837,199
; PRIOR FILING DATE: 1997-04-14
; PRIOR APPLICATION NUMBER: US 60/015,907
; PRIOR FILING DATE: 1996-04-22
; PRIOR APPLICATION NUMBER: US 60/017,221
; PRIOR FILING DATE: 1996-05-09
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 37
; LENGTH: 3209
; TYPE: DNA
; ORGANISM: HUMAN
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1091)..(1091)
; OTHER INFORMATION: N in position 1091 indicates any nucleic acid.
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (2078)..(2078)
; OTHER INFORMATION: N in position 2078 indicates a position of divergence between ;
; OTHER INFORMATION: ferent receptor clones.
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (2256)..(2294)
; OTHER INFORMATION: N in positions 2256 to 2294 indicates positions of divergence ;
; OTHER INFORMATION: ween different receptor clones.
US-10-155-693-37

Query Match      12.4%; Score 31; DB 12; Length 3209;
Best Local Similarity 100.0%; Pred. No. 7.2e-07;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 94 AAAATCNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 124
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Db 2300 AAAATCNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 2270

RESULT 9
US-10-205-951-36
; Sequence 36, Application: US/10205951
; Publication No. US20030119026A1
; GENERAL INFORMATION:

```

APPLICANT: Le, Wei-dong  
APPLICANT: Vassilatis, Demetrios K  
TITLE OF INVENTION: Mutant Nurr1 Gene in Parkinson's Disease  
FILE REFERENCE: P02512US1  
CURRENT APPLICATION NUMBER: US/10/205,951  
CURRENT FILING DATE: 2002-07-26

PRIOR APPLICATION NUMBER: US 60/308,294  
PRIOR FILING DATE: 2001-07-27

NUMBER OF SEQ ID NOS: 124

SOFTWARE: PatentIn version 3.1

SEQ ID NO 36

LENGTH: 112

TYPE: DNA

ORGANISM: Human

FEATURE:

NAME/KEY: misc\_feature

LOCATION: (1)..(112)

OTHER INFORMATION: n = deleted nucleotide

JS-10-205-951-36

Query Match 12.0%; Score 30; DB 14; Length 112;

Best Local Similarity 100.0%; Pred. No. 2.2e-06;

Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y 100 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNTTCCA 129

bb 68 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNTTCCA 97

RESULT 10

JS-09-833-381-524/c

Sequence 524, Application US/09833381

Patent No. US2002013209CA1

GENERAL INFORMATION:

APPLICANT: Robison, Keith E.

TITLE OF INVENTION: No. US20020132090A1el Nucleic Acid and Protein Homologs

FILE REFERENCE: 5800-119

CURRENT APPLICATION NUMBER: US/09/833,381

CURRENT FILING DATE: 2001-04-11

PRIOR APPLICATION NUMBER: 09/516,448

PRIOR FILING DATE: 2000-02-29

NUMBER OF SEQ ID NOS: 2050

SOFTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO 524

LENGTH: 278

TYPE: DNA

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: misc\_feature

LOCATION: (1)..(278)

OTHER INFORMATION: n = A,T,C or G

S-09-833-381-524

Query Match 12.0%; Score 30; DB 10; Length 278;

Best Local Similarity 100.0%; Pred. No. 2.3e-06;

Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y 95 AAATCNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 124

b 33 AAATCNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 4

ESULT 11

S-10-027-632-286679/c

Sequence 286679, Application US/10027632

Publication No. US20030204075A9

GENERAL INFORMATION:

APPLICANT: Wang, David G.

TITLE OF INVENTION: Identification and Mapping of Single Nucleotide

FILE REFERENCE: 108827.129

CURRENT APPLICATION NUMBER: US/10/027,632

CURRENT FILING DATE: 2002-04-30

; PRIOR APPLICATION NUMBER: US 60/218,006

; PRIOR FILING DATE: 2000-07-12

; PRIOR APPLICATION NUMBER: US 60/198,676

; PRIOR FILING DATE: 2000-04-20

; PRIOR APPLICATION NUMBER: US 60/193,483

; PRIOR FILING DATE: 2000-03-29

; PRIOR APPLICATION NUMBER: US 60/185,218

; PRIOR FILING DATE: 2000-02-24

; PRIOR APPLICATION NUMBER: US 60/167,363

; PRIOR FILING DATE: 1999-11-23

; PRIOR APPLICATION NUMBER: US 60/156,358

; PRIOR FILING DATE: 1999-09-28

; PRIOR APPLICATION NUMBER: US 60/146,002

; NUMBER OF SEQ ID NOS: 325720

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 286679

; LENGTH: 583

; TYPE: DNA

; ORGANISM: Human

; FEATURE:

; NAME/KEY: misc\_feature

; LOCATION: (1)..(583)

; OTHER INFORMATION: n = A,T,C or G

US-10-027-632-286679

Query Match 12.0%; Score 30; DB 12; Length 583;

Best Local Similarity 100.0%; Pred. No. 2.4e-06;

Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 100 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNTTCCA 129

Db 564 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNTTCCA 535

RESULT 12

US-10-027-632-286679/c

; Sequence 286679, Application US/10027632

; GENERAL INFORMATION:

; APPLICANT: Wang, David G.

; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide

; FILE REFERENCE: 108827.129

; CURRENT APPLICATION NUMBER: US/10/027,632

; CURRENT FILING DATE: 2002-04-30

; PRIOR APPLICATION NUMBER: US 60/218,006

; PRIOR FILING DATE: 2000-07-12

; PRIOR APPLICATION NUMBER: US 60/198,676

; PRIOR FILING DATE: 2000-04-20

; PRIOR APPLICATION NUMBER: US 60/193,483

; PRIOR FILING DATE: 2000-03-29

; PRIOR APPLICATION NUMBER: US 60/185,218

; PRIOR FILING DATE: 2000-02-24

; PRIOR APPLICATION NUMBER: US 60/167,363

; PRIOR FILING DATE: 1999-11-23

; PRIOR APPLICATION NUMBER: US 60/156,358

; PRIOR FILING DATE: 1999-09-28

; PRIOR APPLICATION NUMBER: US 60/146,002

; NUMBER OF SEQ ID NOS: 325720

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 286679

; LENGTH: 583

; TYPE: DNA

; ORGANISM: Human

; FEATURE:

; NAME/KEY: misc\_feature

; LOCATION: (1)..(583)

; OTHER INFORMATION: n = A,T,C or G

US-10-027-632-286679

Query Match 12.0%; Score 30; DB 13; Length 583;

Best Local Similarity 100.0%; Pred. No. 2.4e-06;



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M nucleic - nucleic search, using sw model

Run on: November 6, 2003, 04:11:09 ; Search time 1320 Seconds  
(without alignments)  
4621.533 Million cell updates/sec

Title: US-09-960-481-5278  
Perfect score: 251  
Sequence: 1 ggtggcagttgtgtgacaca.....gtaagaaganatcaaccgag 251

Coring table: OLIGO\_NUC  
Gapop 60.0 , Gapext 60.0

Searched: 22781392 seqs, 12152238056 residues

Word size : 0

Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database : EST:

- 1: em\_estba:\*
- 2: em\_esthum:\*
- 3: em\_estin:\*
- 4: em\_estmu:\*
- 5: em\_estov:\*
- 6: em\_estpl:\*
- 7: em\_estro:\*
- 8: em\_htc:\*
- 9: gb\_est1:\*
- 10: gb\_est2:\*
- 11: gb\_htc:\*
- 12: gb\_est3:\*
- 13: gb\_est4:\*
- 14: gb\_est5:\*
- 15: em\_estfun:\*
- 16: em\_estom:\*
- 17: em\_gss\_hum:\*
- 18: em\_gss\_inv:\*
- 19: em\_gss\_pln:\*
- 20: em\_gss\_vrt:\*
- 21: em\_gss\_fun:\*
- 22: em\_gss\_mam:\*
- 23: em\_gss\_mus:\*
- 24: em\_gss\_pro:\*
- 25: em\_gss\_rod:\*
- 26: em\_gss\_phg:\*
- 27: em\_gss\_vrl:\*
- 28: gb\_gss1:\*
- 29: gb\_gss2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

result No.	Score	Query Match	Length	DB ID	Description
1	116	46.2	218	13	BU764411
2	116	46.2	389	10	BF068522
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					BU764411 sas01a10.
					BF068522 st83b03.Y
					BU090931 su09e10.Y
					BG041196 sv31a02.Y

C 78 31 12.4 377 12 BI472052 sah98g11.  
C 79 31 12.4 382 14 CB808955 AMGNNUC:M  
80 31 12.4 382 14 CB809376 AMGNNUC:T  
81 31 12.4 385 12 BM341244 MEST332-D  
C 82 31 12.4 388 14 CB805546 AMGNNUC:S  
C 83 31 12.4 396 14 CB773375 AMGNNUC:S  
84 31 12.4 397 14 CB707903 AMGNNUC:S  
85 31 12.4 401 14 CB698694 AMGNNUC:S  
86 31 12.4 403 14 CB812368 AMGNNUC:N  
C 87 31 12.4 404 14 CB811546 AMGNNUC:S  
88 31 12.4 405 14 CB808842 AMGNNUC:N  
C 89 31 12.4 410 14 CB803532 AMGNNUC:N  
C 90 31 12.4 412 14 CB801678 AMGNNUC:S  
91 31 12.4 415 14 CB800390 AMGNNUC:M  
C 92 31 12.4 424 14 CB796841 AMGNNUC:N  
C 93 31 12.4 428 14 CB762449 AMGNNUC:N  
C 94 31 12.4 429 14 CB762353 AMGNNUC:N  
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C 98 31 12.4 437 14 CB791124 AMGNNUC:N  
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105 31 12.4 443 14 CB789256 AMGNNUC:S  
C 106 31 12.4 444 14 CB745447 AMGNNUC:N  
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108 31 12.4 448 14 CB745920 AMGNNUC:M  
C 109 31 12.4 448 14 CB746230 AMGNNUC:N  
C 110 31 12.4 450 14 CB742041 AMGNNUC:N  
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113 31 12.4 453 14 CB785548 AMGNNUC:M  
114 31 12.4 453 14 CB785643 AMGNNUC:N  
115 31 12.4 456 14 CB740839 AMGNNUC:N  
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117 31 12.4 460 14 CB737801 AMGNNUC:M  
118 31 12.4 461 14 CB737069 AMGNNUC:M  
119 31 12.4 461 14 CB737070 AMGNNUC:M  
C 120 31 12.4 470 14 CB733464 AMGNNUC:N  
121 31 12.4 471 14 CB732854 AMGNNUC:M  
122 31 12.4 481 14 CB728226 AMGNNUC:N  
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C 125 31 12.4 496 14 CB712927 AMGNNUC:N  
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C 127 31 12.4 508 11 AY112346 Zea mays  
128 31 12.4 514 14 CB716658 AMGNNUC:S  
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C 130 31 12.4 547 14 CB611484 AMGNNUC:S  
131 31 12.4 564 14 CB608857 AMGNNUC:S  
C 132 31 12.4 577 13 BU937181 AGENCOURT  
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C 136 31 12.4 642 11 AY111523 Zea mays  
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138 31 12.4 653 13 BU203050 604153296  
139 31 12.4 656 11 AY110723 Zea mays  
C 140 31 12.4 664 13 BU523671 AGENCOURT  
C 141 31 12.4 666 28 B19475 TSN17-T7 TA  
142 31 12.4 683 14 CB556669 AMGNNUC:U  
C 143 31 12.4 745 12 BM474479 AGENCOURT  
C 144 31 12.4 837 12 BM552063 AGENCOURT  
C 145 31 12.4 877 11 AY111658 Zea mays  
C 146 31 12.4 882 13 BU589046 AGENCOURT  
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C 148 31 12.4 1209 11 AY109337 Zea mays  
C 149 31 12.4 2474 11 AY110115 Zea mays  
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C 151 30 12.0 292 14 CB710100 AMGNNUC:N  
C 152 30 12.0 327 12 BM267776 MEST372-A  
C 153 30 12.0 347 14 CB705221 AMGNNUC:Y  
154 30 12.0 356 14 CB813713 AMGNNUC:S  
C 155 30 12.0 357 14 CB813006 AMGNNUC:N  
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C 157 30 12.0 375 14 CB691732 AMGNNUC:S  
158 30 12.0 383 14 CB808920 AMGNNUC:M  
C 159 30 12.0 385 14 CB702364 AMGNNUC:S  
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C 161 30 12.0 394 14 CB782281 AMGNNUC:H  
C 162 30 12.0 399 14 CB706801 AMGNNUC:N  
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C 225	30	12.0	456	14	CB741014	CB741014 AMGNNUC:N
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C 227	30	12.0	458	12	BQ049078	BQ049078 AGENCOURT
C 228	30	12.0	458	14	CB738912	CB738912 AMGNNUC:N
C 229	30	12.0	458	14	CB739318	CB739318 AMGNNUC:N
C 230	30	12.0	459	14	CB738723	CB738723 AMGNNUC:M
C 231	30	12.0	460	14	CB605719	CB605719 AMGNNUC:M
C 232	30	12.0	460	14	CB738102	CB738102 AMGNNUC:M
C 233	30	12.0	461	14	CB737134	CB737134 AMGNNUC:N
C 234	30	12.0	462	14	CB736551	CB736551 AMGNNUC:M
C 235	30	12.0	464	13	BU943807	BU943807 AGENCOURT
C 236	30	12.0	464	14	CB734626	CB734626 AMGNNUC:M
C 237	30	12.0	466	14	CB714668	CB714668 AMGNNUC:N
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C 240	30	12.0	469	14	CB733616	CB733616 AMGNNUC:M
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C 242	30	12.0	471	14	CB732834	CB732834 AMGNNUC:N
C 243	30	12.0	472	14	CB730312	CB730312 AMGNNUC:N
C 244	30	12.0	473	14	CB729784	CB729784 AMGNNUC:N
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C 246	30	12.0	480	14	CB730761	CB730761 AMGNNUC:N
C 247	30	12.0	484	14	CB727422	CB727422 AMGNNUC:S
C 248	30	12.0	485	14	CB727254	CB727254 AMGNNUC:N
C 249	30	12.0	486	14	CB726716	CB726716 AMGNNUC:N
C 250	30	12.0	489	14	CB725903	CB725903 AMGNNUC:N
C 251	30	12.0	490	14	CB725829	CB725829 AMGNNUC:T
C 252	30	12.0	495	13	BQ490657	BQ490657 19-E9134-
C 253	30	12.0	496	13	BU566201	BU566201 AGENCOURT
C 254	30	12.0	499	14	CB712410	CB712410 AMGNNUC:C
C 255	30	12.0	501	14	CB711928	CB711928 AMGNNUC:U
C 256	30	12.0	506	9	AI996752	AI996752 701668236
C 257	30	12.0	516	13	BU179630	BU179630 AGENCOURT
C 258	30	12.0	522	13	BU842541	BU842541 AGENCOURT
C 259	30	12.0	522	14	CB547859	CB547859 AMGNNUC:N
C 260	30	12.0	524	14	H15567	H15567 YM27906.81
C 261	30	12.0	538	14	CB717432	CB717432 AMGNNUC:N
C 262	30	12.0	547	14	CB611480	CB611480 AMGNNUC:S
C 263	30	12.0	549	14	CB614742	CB614742 AMGNNUC:S
C 264	30	12.0	558	13	BU170823	BU170823 AGENCOURT
C 265	30	12.0	561	13	BU927700	BU927700 AGENCOURT
C 266	30	12.0	566	13	BU349082	BU349082 604171508
C 267	30	12.0	567	13	BQ680045	BQ680045 AGENCOURT
C 268	30	12.0	572	13	BU199957	BU199957 604154237
C 269	30	12.0	575	14	CB608071	CB608071 AMGNNUC:C
C 270	30	12.0	586	11	AY111527	AY111527 Zea mays
C 271	30	12.0	587	14	CB585351	CB585351 AMGNNUC:U
C 272	30	12.0	590	14	CB583641	CB583641 AMGNNUC:N
C 273	30	12.0	593	14	CB584413	CB584413 AMGNNUC:N
C 274	30	12.0	602	14	CB582118	CB582118 AMGNNUC:S
C 275	30	12.0	606	14	CB581346	CB581346 AMGNNUC:N
C 276	30	12.0	613	14	CA741402	CA741402 wialc.pk0
C 277	30	12.0	615	13	BQ072464	BQ072464 AGENCOURT
C 278	30	12.0	621	11	AY110363	AY110363 Zea mays
C 279	30	12.0	623	13	BU848039	BU848039 AGENCOURT
C 280	30	12.0	624	14	CB578292	CB578292 AMGNNUC:S
C 281	30	12.0	628	13	BQ228319	BQ228319 AGENCOURT
C 282	30	12.0	632	13	BU182480	BU182480 AGENCOURT
C 283	30	12.0	638	13	BU161381	BU161381 AGENCOURT
C 284	30	12.0	640	13	BU860762	BU860762 AGENCOURT
C 285	30	12.0	641	11	AY111029	AY111029 Zea mays
C 286	30	12.0	641	13	BU961267	BU961267 AGENCOURT
C 287	30	12.0	644	14	CB576214	CB576214 AMGNNUC:S
C 288	30	12.0	650	13	BU292429	BU292429 604166118
C 289	30	12.0	655	11	AY110518	AY110518 Zea mays
C 290	30	12.0	658	13	BQ678921	BQ678921 AGENCOURT
C 291	30	12.0	661	11	AY112329	AY112329 Zea mays
C 292	30	12.0	665	28	AZ527391	AZ527391 267PbA05
C 293	30	12.0	666	14	CB781548	CB781548 AMGNNUC:N
C 294	30	12.0	672	13	BU406808	BU406808 604138022
C 295	30	12.0	685	14	CB556651	CB556651 AMGNNUC:Y
C 296	30	12.0	686	14	CB556616	CB556616 AMGNNUC:Y

688	13	688	13	BU208148	BU208148
691	11	691	11	AY111071	AY111071 Zea mays
701	28	701	28	AZ132431	AZ132431 OSJNBb006
708	29	708	29	AG045940	AG045940 Pan trogl
726	12	726	12	BM550939	BM550939 AGENCOURT
730	13	730	13	BU955987	BU955987 AGENCOURT
732	12	732	12	BI885751	BI885751 ZF637-1-0
732	12	732	12	BM550333	BM550333 AGENCOURT
733	12	733	12	BM915584	BM915584 AGENCOURT
757	29	757	29	CC313852	CC313852 TAM32-23B
759	12	759	12	BM559074	BM559074 AGENCOURT
767	12	767	12	BI887945	BI887945 ZF637-1-0
769	13	769	13	BU211897	BU211897 604156588
778	13	778	13	BU557518	BU557518 AGENCOURT
820	14	820	14	CB587576	CB587576 AGENCOURT
822	13	822	13	BU955562	BU955562 AGENCOURT
823	14	823	14	CB319085	CB319085 AGENCOURT
826	14	826	14	CA466527	CA466527 AGENCOURT
829	13	829	13	BU557569	BU557569 AGENCOURT
839	11	839	11	AY110457	AY110457 Zea mays
845	14	845	14	CA494546	CA494546 AGENCOURT
858	13	858	13	BU860780	BU860780 AGENCOURT
896	13	896	13	BQ219362	BQ219362 AGENCOURT
901	13	901	13	BU960890	BU960890 AGENCOURT
915	13	915	13	BU167748	BU167748 AGENCOURT
919	13	919	13	BQ220131	BQ220131 AGENCOURT
932	13	932	13	BU905290	BU905290 AGENCOURT
936	13	936	13	BU953714	BU953714 AGENCOURT
946	13	946	13	BQ691840	BQ691840 AGENCOURT
952	14	952	14	CA981788	CA981788 AGENCOURT
955	13	955	13	BQ423361	BQ423361 AGENCOURT
967	11	967	11	AY112367	AY112367 Zea mays
1022	11	1022	11	AY110438	AY110438 Zea mays
1062	11	1062	11	AY110203	AY110203 Zea mays
1069	11	1069	11	AY112592	AY112592 Zea mays
1097	12	1097	12	BM805283	BM805283 AGENCOURT
1131	29	1131	29	CC304186	CC304186 CH261-52J
1135	29	1135	29	CC304191	CC304191 CH261-52J
1251	29	1251	29	CC268218	CC268218 CH261-88L
1318	29	1318	29	CC188209	CC188209 CH261-38O
1324	14	1324	14	CB206108	CB206108 AGENCOURT
1373	29	1373	29	CC235146	CC235146 CH261-169
1387	29	1387	29	CC212250	CC212250 CH261-170
1448	29	1448	29	CC185035	CC185035 CH261-17D
1450	29	1450	29	CC210982	CC210982 CH261-170
1465	29	1465	29	CC289673	CC289673 CH261-171
1480	29	1480	29	CC297119	CC297119 CH261-177
1523	29	1523	29	CC194564	CC194564 CH261-170
1545	29	1545	29	CC288560	CC288560 CH261-170
1604	29	1604	29	CC246351	CC246351 CH261-36O
1671	14	1671	14	CA993999	CA993999 A1126 Pst
1722	11	1722	11	AY109704	AY109704 Zea mays
2590	11	2590	11	AY109999	AY109999 Zea mays
3459	11	3459	11	AY110274	AY110274 Zea mays
155	29	155	29	AL947166	AL947166 Arabidops
186	11	186	11	AY112556	AY112556 Zea mays
236	29	236	29	BX288589	BX288589 Arabidops
239	13	239	13	BU812742	BU812742 UL64PH03
259	29	259	29	CC466898	CC466898 CH240 136
282	14	282	14	CB547768	CB547768 AMGNNUC:N
287	14	287	14	CB710982	CB710982 AMGNNUC:N
291	14	291	14	CB710264	CB710264 AMGNNUC:N
296	13	296	13	BU443795	BU443795 604142567
299	14	299	14	CB701239	CB701239 AMGNNUC:N
300	14	300	14	CB701087	CB701087 AMGNNUC:M
301	14	301	14	CB700803	CB700803 AMGNNUC:N
301	14	301	14	CB700829	CB700829 AMGNNUC:N
301	14	301	14	CB700905	CB700905 AMGNNUC:C
310	14	310	14	CB697072	CB697072 AMGNNUC:N
310	14	310	14	CB697116	CB697116 AMGNNUC:C
320	14	320	14	CB707973	CB707973 AMGNNUC:T
334	29	334	29	BX532968	BX532968 Arabidops
335	14	335	14	CB547298	CB547298 AMGNNUC:S



C 370	29	11.6	344	12	BI887933	BI887933	ZF637-1-0	443	29	11.6	408	14	CB771084	CB771084	AMGNNUC:S
371	29	11.6	349	13	C9781401	CB781401	AMGNNUC:U	444	29	11.6	408	14	CB771140	CB771140	AMGNNUC:S
C 372	29	11.6	356	13	BQ423453	BQ423453	AGENCOURT	C 445	29	11.6	409	14	CB805012	CB805012	AMGNNUC:N
C 373	29	11.6	356	14	CB813717	CB813717	AMGNNUC:S	446	29	11.6	409	14	CB805042	CB805042	AMGNNUC:S
374	29	11.6	358	14	CB812857	CB812857	AMGNNUC:H	C 447	29	11.6	409	14	CB805042	CB805042	AMGNNUC:S
375	29	11.6	375	13	BU963392	BU963392	AGENCOURT	C 448	29	11.6	410	13	BU960114	BU960114	AGENCOURT
C 376	29	11.6	375	14	CB691577	CB691577	AMGNNUC:S	C 449	29	11.6	410	14	CB803687	CB803687	AMGNNUC:S
C 377	29	11.6	376	14	CB691130	CB691130	AMGNNUC:N	450	29	11.6	410	14	CB804127	CB804127	AMGNNUC:N
378	29	11.6	376	14	CB691175	CB691175	AMGNNUC:M	C 451	29	11.6	411	14	CB803085	CB803085	AMGNNUC:M
379	29	11.6	376	14	CB782353	CB782353	AMGNNUC:C	452	29	11.6	411	14	CB803086	CB803086	AMGNNUC:N
380	29	11.6	380	14	CB810241	CB810241	AMGNNUC:S	453	29	11.6	412	14	CB801630	CB801630	AMGNNUC:N
C 381	29	11.6	380	14	CB810567	CB810567	AMGNNUC:S	C 454	29	11.6	415	14	CB800292	CB800292	AMGNNUC:M
382	29	11.6	382	29	BX286979	BX286979	Arabidops	C 455	29	11.6	415	14	CB800588	CB800588	AMGNNUC:S
383	29	11.6	383	14	CB704080	CB704080	AMGNNUC:S	456	29	11.6	415	14	CB800873	CB800873	AMGNNUC:C
C 384	29	11.6	383	14	CB704166	CB704166	AMGNNUC:N	C 457	29	11.6	416	13	BU960872	BU960872	AGENCOURT
385	29	11.6	384	14	CB703101	CB703101	AMGNNUC:N	458	29	11.6	416	14	CB767508	CB767508	AMGNNUC:Y
386	29	11.6	384	14	CB703525	CB703525	AMGNNUC:M	459	29	11.6	416	14	CB767738	CB767738	AMGNNUC:N
387	29	11.6	384	29	AL950592	AL950592	Arabidops	460	29	11.6	416	14	CB768060	CB768060	AMGNNUC:N
C 388	29	11.6	387	14	CB806188	CB806188	AMGNNUC:S	461	29	11.6	417	11	AY112507	AY112507	Zea mays
C 389	29	11.6	387	14	CB806199	CB806199	AMGNNUC:N	C 462	29	11.6	417	14	CB766771	CB766771	AMGNNUC:N
C 390	29	11.6	388	14	CB805573	CB805573	AMGNNUC:M	463	29	11.6	417	14	CB767136	CB767136	AMGNNUC:N
C 391	29	11.6	388	14	CB805583	CB805583	AMGNNUC:M	464	29	11.6	417	14	CB767282	CB767282	AMGNNUC:S
C 392	29	11.6	389	14	CB778716	CB778716	AMGNNUC:S	465	29	11.6	417	14	CB767361	CB767361	AMGNNUC:N
C 393	29	11.6	389	14	CB778756	CB778756	AMGNNUC:S	466	29	11.6	418	14	CB765482	CB765482	AMGNNUC:N
394	29	11.6	389	14	CB778776	CB778776	AMGNNUC:C	C 467	29	11.6	418	14	CB765607	CB765607	AMGNNUC:S
395	29	11.6	389	14	CB779222	CB779222	AMGNNUC:S	468	29	11.6	418	14	CB765786	CB765786	AMGNNUC:N
C 396	29	11.6	389	14	CB779222	CB779222	AMGNNUC:S	C 469	29	11.6	418	14	CB766123	CB766123	AMGNNUC:S
397	29	11.6	390	14	CB777782	CB777782	AMGNNUC:N	C 470	29	11.6	419	14	CB764895	CB764895	AMGNNUC:N
398	29	11.6	390	14	CB777896	CB777896	AMGNNUC:N	C 471	29	11.6	419	14	CB799478	CB799478	AMGNNUC:N
C 399	29	11.6	390	14	CB778077	CB778077	AMGNNUC:N	472	29	11.6	420	14	CB798307	CB798307	AMGNNUC:N
C 400	29	11.6	390	14	CB778499	CB778499	AMGNNUC:N	473	29	11.6	420	14	CB798574	CB798574	AMGNNUC:N
401	29	11.6	391	14	CB775618	CB775618	AMGNNUC:S	C 474	29	11.6	420	14	CB798706	CB798706	AMGNNUC:N
402	29	11.6	392	14	CB774641	CB774641	AMGNNUC:S	C 475	29	11.6	420	14	CB798748	CB798748	AMGNNUC:N
403	29	11.6	392	14	CB775033	CB775033	AMGNNUC:N	C 476	29	11.6	420	14	CB799003	CB799003	AMGNNUC:N
404	29	11.6	392	14	CB775066	CB775066	AMGNNUC:M	C 477	29	11.6	421	14	CA494607	CA494607	AGENCOURT
405	29	11.6	393	14	CB774197	CB774197	AMGNNUC:S	478	29	11.6	421	14	CB764229	CB764229	AMGNNUC:N
406	29	11.6	393	14	CB774198	CB774198	AMGNNUC:S	479	29	11.6	421	14	CB764416	CB764416	AMGNNUC:N
C 407	29	11.6	394	14	CB776785	CB776785	AMGNNUC:N	480	29	11.6	421	14	CB797570	CB797570	AMGNNUC:N
C 408	29	11.6	395	12	BM281734	BM281734	ki19g06.y	C 481	29	11.6	421	14	CB797681	CB797681	AMGNNUC:N
C 409	29	11.6	395	14	CB773588	CB773588	AMGNNUC:U	C 482	29	11.6	421	14	AL769168	AL769168	Arabidops
C 410	29	11.6	395	14	CB773780	CB773780	AMGNNUC:N	C 483	29	11.6	422	13	BU531732	BU531732	AGENCOURT
C 411	29	11.6	395	14	CB776143	CB776143	AMGNNUC:T	C 484	29	11.6	422	14	CB763220	CB763220	AMGNNUC:N
412	29	11.6	395	14	CB776285	CB776285	AMGNNUC:S	485	29	11.6	422	14	CB763538	CB763538	AMGNNUC:N
413	29	11.6	396	14	CB772739	CB772739	AMGNNUC:S	486	29	11.6	422	14	CB763931	CB763931	AMGNNUC:N
414	29	11.6	399	14	CB706336	CB706336	AMGNNUC:M	C 487	29	11.6	423	14	CB762757	CB762757	AMGNNUC:N
415	29	11.6	399	14	CB706774	CB706774	AMGNNUC:N	488	29	11.6	423	14	CB796941	CB796941	AMGNNUC:S
416	29	11.6	399	14	CB782267	CB782267	AMGNNUC:H	C 489	29	11.6	423	14	CB796944	CB796944	AMGNNUC:S
C 417	29	11.6	400	14	CB544380	CB544380	AMGNNUC:N	C 490	29	11.6	423	14	CB796951	CB796951	AMGNNUC:N
C 418	29	11.6	400	14	CB699736	CB699736	AMGNNUC:M	C 491	29	11.6	423	14	CB797160	CB797160	AMGNNUC:M
C 419	29	11.6	401	14	CB769994	CB769994	AMGNNUC:S	C 492	29	11.6	424	14	CB795963	CB795963	AMGNNUC:N
420	29	11.6	401	14	CB770030	CB770030	AMGNNUC:S	C 493	29	11.6	424	14	CB796057	CB796057	AMGNNUC:N
421	29	11.6	402	14	CB769674	CB769674	AMGNNUC:N	494	29	11.6	424	14	CB796197	CB796197	AMGNNUC:N
C 422	29	11.6	402	14	CB769789	CB769789	AMGNNUC:M	C 495	29	11.6	425	14	CB696022	CB696022	AMGNNUC:M
C 423	29	11.6	402	29	AL763221	AL763221	Arabidops	496	29	11.6	425	14	CB696361	CB696361	AMGNNUC:N
C 424	29	11.6	403	14	CB768244	CB768244	AMGNNUC:N	C 497	29	11.6	425	14	CB696409	CB696409	AMGNNUC:S
425	29	11.6	403	14	CB768443	CB768443	AMGNNUC:N	498	29	11.6	425	14	CB795842	CB795842	AMGNNUC:M
426	29	11.6	403	14	CB768644	CB768644	AMGNNUC:S	499	29	11.6	426	14	CB695390	CB695390	AMGNNUC:N
427	29	11.6	403	14	CB768824	CB768824	AMGNNUC:M	500	29	11.6	427	12	BM078430	BM078430	MEST119-B
428	29	11.6	405	14	CB808523	CB808523	AMGNNUC:N	C 501	29	11.6	427	14	CB794692	CB794692	AMGNNUC:N
C 429	29	11.6	405	14	CB808544	CB808544	AMGNNUC:N	C 502	29	11.6	427	14	CB794770	CB794770	AMGNNUC:N
430	29	11.6	405	14	CB808554	CB808554	AMGNNUC:S	503	29	11.6	427	14	CB794785	CB794785	AMGNNUC:N
C 431	29	11.6	405	14	CB808627	CB808627	AMGNNUC:N	C 504	29	11.6	427	14	CB794892	CB794892	AMGNNUC:U
432	29	11.6	405	14	CB810881	CB810881	AMGNNUC:N	505	29	11.6	427	14	CB795075	CB795075	AMGNNUC:N
433	29	11.6	405	14	CB811078	CB811078	AMGNNUC:S	C 506	29	11.6	428	14	CB794021	CB794021	AMGNNUC:N
434	29	11.6	405	14	CB811278	CB811278	AMGNNUC:N	C 507	29	11.6	428	14	CB794464	CB794464	AMGNNUC:S
435	29	11.6	406	14	CB807477	CB807477	AMGNNUC:C	C 508	29	11.6	428	14	CB794478	CB794478	AMGNNUC:N
436	29	11.6	406	14	CB808186	CB808186	AMGNNUC:N	C 509	29	11.6	428	14	CB794484	CB794484	AMGNNUC:S
C 437	29	11.6	406	14	CB808450	CB808450	AMGNNUC:Y	510	29	11.6	428	14	CB794541	CB794541	AMGNNUC:M
438	29	11.6	407	14	CB771387	CB771387	AMGNNUC:N	C 511	29	11.6	428	14	CB794585	CB794585	AMGNNUC:N
439	29	11.6	407	14	CB771662	CB771662	AMGNNUC:N	512	29	11.6	430	14	CB758556	CB758556	AMGNNUC:M
C 440	29	11.6	408	14	CB770894	CB770894	AMGNNUC:M	C 513	29	11.6	430	14	CB758659	CB758659	AMGNNUC:N
441	29	11.6	408	14	CB770954	CB770954	AMGNNUC:N	514	29	11.6	430	14	CB760807	CB760807	AMGNNUC:M
442	29	11.6	408	14	CB770976	CB770976	AMGNNUC:N	515	29	11.6	431	14	CB757847	CB757847	AMGNNUC:M



C 516	29	11.6	431	14	CB757883	CB757883	AMGNNUC:N	C 589	29	11.6	449	14	CB742958	CB742958	AMGNNUC:N
C 517	29	11.6	431	14	CB758223	CB758223	AMGNNUC:S	C 590	29	11.6	449	14	CB743037	CB743037	AMGNNUC:N
518	29	11.6	431	14	CB758348	CB758348	AMGNNUC:N	C 591	29	11.6	449	14	CB743143	CB743143	AMGNNUC:N
519	29	11.6	431	14	CB758352	CB758352	AMGNNUC:N	592	29	11.6	449	14	CB743245	CB743245	AMGNNUC:M
C 520	29	11.6	431	14	CB758389	CB758389	AMGNNUC:M	C 593	29	11.6	449	14	CB743389	CB743389	AMGNNUC:S
C 521	29	11.6	432	14	CB757172	CB757172	AMGNNUC:N	594	29	11.6	449	14	CB743396	CB743396	AMGNNUC:S
C 522	29	11.6	432	14	CB760570	CB760570	AMGNNUC:S	595	29	11.6	450	11	AY111591	AY111591	Zea mays
C 523	29	11.6	432	14	CB760603	CB760603	AMGNNUC:S	596	29	11.6	450	14	CB742325	CB742325	AMGNNUC:M
524	29	11.6	433	14	CB759608	CB759608	AMGNNUC:M	C 597	29	11.6	450	14	CB787699	CB787699	AMGNNUC:N
C 525	29	11.6	433	14	CB759889	CB759889	AMGNNUC:N	C 598	29	11.6	450	14	CB787748	CB787748	AMGNNUC:M
C 526	29	11.6	433	14	CB760143	CB760143	AMGNNUC:S	C 599	29	11.6	451	14	CB786888	CB786888	AMGNNUC:N
C 527	29	11.6	433	14	CB760215	CB760215	AMGNNUC:S	C 600	29	11.6	451	14	CB787047	CB787047	AMGNNUC:N
C 528	29	11.6	434	14	CB758816	CB758816	AMGNNUC:N	601	29	11.6	451	14	CB787301	CB787301	AMGNNUC:M
529	29	11.6	434	14	CB759238	CB759238	AMGNNUC:N	602	29	11.6	451	14	CB787398	CB787398	AMGNNUC:N
C 530	29	11.6	434	14	CB759389	CB759389	AMGNNUC:N	C 603	29	11.6	451	14	CB787401	CB787401	AMGNNUC:M
531	29	11.6	434	14	CB793518	CB793518	AMGNNUC:N	604	29	11.6	451	14	CB787431	CB787431	AMGNNUC:M
C 532	29	11.6	434	14	CB793655	CB793655	AMGNNUC:N	605	29	11.6	451	14	CB787467	CB787467	AMGNNUC:N
533	29	11.6	434	14	CB793674	CB793674	AMGNNUC:N	606	29	11.6	451	14	CB787585	CB787585	AMGNNUC:N
C 534	29	11.6	434	14	CB793688	CB793688	AMGNNUC:N	C 607	29	11.6	452	14	CB786462	CB786462	AMGNNUC:N
535	29	11.6	435	9	AI994349	AI994349	701514769	C 608	29	11.6	452	14	CB786555	CB786555	AMGNNUC:N
C 536	29	11.6	435	14	CB793326	CB793326	AMGNNUC:N	C 609	29	11.6	453	14	CB547596	CB547596	AMGNNUC:M
C 537	29	11.6	435	14	CB793327	CB793327	AMGNNUC:N	610	29	11.6	453	14	CB785344	CB785344	AMGNNUC:N
C 538	29	11.6	436	9	AI993421	AI993421	701496255	C 611	29	11.6	453	14	CB785494	CB785494	AMGNNUC:N
539	29	11.6	436	14	CB791913	CB791913	AMGNNUC:N	C 612	29	11.6	453	14	CB785494	CB785494	AMGNNUC:N
540	29	11.6	436	14	CB792173	CB792173	AMGNNUC:N	613	29	11.6	453	14	CB785850	CB785850	AMGNNUC:N
C 541	29	11.6	436	14	CB792290	CB792290	AMGNNUC:S	C 614	29	11.6	453	14	CB785859	CB785859	AMGNNUC:N
542	29	11.6	437	14	CB791003	CB791003	AMGNNUC:M	C 615	29	11.6	453	14	CB785890	CB785890	AMGNNUC:M
543	29	11.6	437	14	CB791095	CB791095	AMGNNUC:N	C 616	29	11.6	455	14	CB785913	CB785913	AMGNNUC:N
C 544	29	11.6	437	14	CB791186	CB791186	AMGNNUC:N	C 617	29	11.6	455	14	CB741311	CB741311	AMGNNUC:N
545	29	11.6	437	14	CB791306	CB791306	AMGNNUC:S	C 618	29	11.6	455	14	CB741435	CB741435	AMGNNUC:M
C 546	29	11.6	438	14	CB751214	CB751214	AMGNNUC:N	C 619	29	11.6	455	14	CB741556	CB741556	AMGNNUC:N
C 547	29	11.6	438	14	CB789974	CB789974	AMGNNUC:N	620	29	11.6	455	14	CB741576	CB741576	AMGNNUC:M
C 548	29	11.6	438	14	CB790241	CB790241	AMGNNUC:N	621	29	11.6	455	14	CB741664	CB741664	AMGNNUC:T
C 549	29	11.6	438	14	CB790393	CB790393	AMGNNUC:N	C 622	29	11.6	455	14	CB741754	CB741754	AMGNNUC:N
C 550	29	11.6	439	14	CB750731	CB750731	AMGNNUC:N	C 623	29	11.6	455	14	CB741893	CB741893	AMGNNUC:M
C 551	29	11.6	440	14	CB749322	CB749322	AMGNNUC:S	624	29	11.6	455	14	CB741927	CB741927	AMGNNUC:N
552	29	11.6	440	14	CB749335	CB749335	AMGNNUC:N	625	29	11.6	456	14	CB606191	CB606191	AMGNNUC:N
553	29	11.6	440	14	CB749465	CB749465	AMGNNUC:N	626	29	11.6	456	14	CB740617	CB740617	AMGNNUC:M
554	29	11.6	440	14	CB749619	CB749619	AMGNNUC:N	C 627	29	11.6	456	14	CB740753	CB740753	AMGNNUC:N
C 555	29	11.6	440	14	CB749703	CB749703	AMGNNUC:N	C 628	29	11.6	456	14	CB740891	CB740891	AMGNNUC:N
C 556	29	11.6	440	14	CB749715	CB749715	AMGNNUC:M	C 629	29	11.6	456	14	CB740978	CB740978	AMGNNUC:N
557	29	11.6	440	14	CB749860	CB749860	AMGNNUC:N	630	29	11.6	456	14	CB782065	CB782065	AMGNNUC:H
558	29	11.6	441	14	CB748104	CB748104	AMGNNUC:N	631	29	11.6	457	14	CA844479	CA844479	hac14e08
C 559	29	11.6	441	14	CB748700	CB748700	AMGNNUC:N	C 632	29	11.6	457	14	CB739617	CB739617	AMGNNUC:M
C 560	29	11.6	442	14	CB747816	CB747816	AMGNNUC:N	C 633	29	11.6	457	14	CB740106	CB740106	AMGNNUC:M
561	29	11.6	442	14	CB789800	CB789800	AMGNNUC:N	C 634	29	11.6	457	14	CB740137	CB740137	AMGNNUC:N
562	29	11.6	442	14	CB789924	CB789924	AMGNNUC:N	C 635	29	11.6	457	14	CB740315	CB740315	AMGNNUC:N
C 563	29	11.6	443	12	BM335644	BM335644	MEST164-F	C 636	29	11.6	457	14	CB740332	CB740332	AMGNNUC:N
C 564	29	11.6	443	14	CB788789	CB788789	AMGNNUC:N	C 637	29	11.6	458	10	AW950730	AW950730	EST362800
565	29	11.6	443	14	CB789001	CB789001	AMGNNUC:N	638	29	11.6	458	13	BU927983	BU927983	AGENCOURT
566	29	11.6	443	14	CB789259	CB789259	AMGNNUC:S	639	29	11.6	458	14	CB739146	CB739146	AMGNNUC:N
C 567	29	11.6	443	14	CB789276	CB789276	AMGNNUC:S	C 640	29	11.6	458	14	CB739513	CB739513	AMGNNUC:N
568	29	11.6	443	14	CB789416	CB789416	AMGNNUC:N	641	29	11.6	459	14	CB738133	CB738133	AMGNNUC:N
569	29	11.6	444	14	CB547164	CB547164	AMGNNUC:S	C 642	29	11.6	459	14	CB738300	CB738300	AMGNNUC:M
570	29	11.6	444	14	CB745492	CB745492	AMGNNUC:M	643	29	11.6	459	14	CB738616	CB738616	AMGNNUC:N
C 571	29	11.6	444	14	CB788282	CB788282	AMGNNUC:M	C 644	29	11.6	459	14	CB738670	CB738670	AMGNNUC:N
C 572	29	11.6	444	14	CB788413	CB788413	AMGNNUC:S	645	29	11.6	459	14	CB738702	CB738702	AMGNNUC:N
573	29	11.6	445	14	CB546295	CB546295	AMGNNUC:N	646	29	11.6	459	14	CB738811	CB738811	AMGNNUC:N
574	29	11.6	445	14	CB744508	CB744508	AMGNNUC:N	C 647	29	11.6	460	13	BQ436070	BQ436070	AGENCOURT
575	29	11.6	445	14	CB744560	CB744560	AMGNNUC:N	648	29	11.6	460	13	BU963308	BU963308	AGENCOURT
C 576	29	11.6	445	14	CB744753	CB744753	AMGNNUC:N	C 649	29	11.6	460	14	CB737485	CB737485	AMGNNUC:N
577	29	11.6	445	14	CB744840	CB744840	AMGNNUC:N	C 650	29	11.6	460	14	CB737575	CB737575	AMGNNUC:N
C 578	29	11.6	445	14	CB745085	CB745085	AMGNNUC:M	651	29	11.6	460	14	CB738117	CB738117	AMGNNUC:N
C 579	29	11.6	446	14	CB743913	CB743913	AMGNNUC:N	C 652	29	11.6	461	9	AL720197	AL720197	AL720197
C 580	29	11.6	446	14	CB744100	CB744100	AMGNNUC:M	C 653	29	11.6	461	13	BU953555	BU953555	AGENCOURT
581	29	11.6	446	14	CB747351	CB747351	AMGNNUC:M	C 654	29	11.6	462	14	CB736611	CB736611	AMGNNUC:N
582	29	11.6	446	14	CB747383	CB747383	AMGNNUC:N	655	29	11.6	462	14	CB736646	CB736646	AMGNNUC:N
583	29	11.6	446	14	CB747512	CB747512	AMGNNUC:N	C 656	29	11.6	463	14	CB735281	CB735281	AMGNNUC:N
C 584	29	11.6	447	14	CB746367	CB746367	AMGNNUC:N	657	29	11.6	464	14	CB734646	CB734646	AMGNNUC:N
C 585	29	11.6	447	14	CB746668	CB746668	AMGNNUC:N	C 658	29	11.6	464	14	CB734749	CB734749	AMGNNUC:N
C 586	29	11.6	447	14	CB746788	CB746788	AMGNNUC:N	659	29	11.6	464	14	CB735267	CB735267	AMGNNUC:M
587	29	11.6	448	14	CB745962	CB745962	AMGNNUC:N	C 660	29	11.6	464	28	AQ151714	AQ151714	HS 3095-A
588	29	11.6	449	14	CB742767	CB742767	AMGNNUC:Y	661	29	11.6	465	14	CB715134	CB715134	AMGNNUC:N

C 662	29	11.6	465	14	CB715508	CB715508 AMGNNUC:N	C 735	29	11.6	528	14	CB719573	CB719573 AMGNNUC:N
663	29	11.6	466	14	CB714611	AMGNNUC:M	C 736	29	11.6	530	13	BU943640	AGENCOURT
664	29	11.6	466	14	CB714832	AMGNNUC:N	737	29	11.6	531	14	CB718868	AMGNNUC:S
C 665	29	11.6	466	14	CB714901	AMGNNUC:M	C 738	29	11.6	533	13	BU554666	AGENCOURT
666	29	11.6	467	14	CB714074	AMGNNUC:N	739	29	11.6	534	14	CB545130	AMGNNUC:C
667	29	11.6	468	14	CB734128	AMGNNUC:M	C 740	29	11.6	534	14	CB718397	AMGNNUC:N
C 668	29	11.6	468	14	CB734147	AMGNNUC:N	741	29	11.6	536	13	BU942831	AGENCOURT
C 669	29	11.6	468	14	CB734338	AMGNNUC:N	C 742	29	11.6	537	13	BU535297	AGENCOURT
670	29	11.6	468	14	CB782026	AMGNNUC:Y	C 743	29	11.6	537	14	CB717626	AMGNNUC:N
671	29	11.6	469	13	BU534830	AGENCOURT	744	29	11.6	540	11	AY112542	Zea mays
C 672	29	11.6	469	14	CB733557	AMGNNUC:N	C 745	29	11.6	540	14	CB612767	AMGNNUC:U
C 673	29	11.6	469	14	CB733595	AMGNNUC:M	C 746	29	11.6	546	28	AZ188223	SP_1011_B
674	29	11.6	469	14	CB733642	AMGNNUC:N	C 747	29	11.6	550	13	BQ688334	AGENCOURT
675	29	11.6	469	14	CB733705	AMGNNUC:N	748	29	11.6	552	14	CB614192	AMGNNUC:S
C 676	29	11.6	470	14	CB733013	AMGNNUC:M	749	29	11.6	553	14	CB613860	AMGNNUC:U
677	29	11.6	470	14	CB733079	AMGNNUC:N	C 750	29	11.6	553	14	CB613963	AMGNNUC:S
678	29	11.6	471	14	CB7330645	AMGNNUC:S	C 751	29	11.6	553	14	CB614027	AMGNNUC:N
C 679	29	11.6	471	14	CB732803	AMGNNUC:N	C 752	29	11.6	554	9	AL963278	AL963278
C 680	29	11.6	472	14	CB546951	AMGNNUC:N	C 753	29	11.6	555	29	AG016512	Homo sapi
C 681	29	11.6	472	14	CB733045C	AMGNNUC:N	754	29	11.6	558	14	CB610282	AMGNNUC:S
682	29	11.6	473	14	CB72986C	AMGNNUC:Y	755	29	11.6	559	12	BI893235	sai63b12..
683	29	11.6	474	9	AI994429	AI994429 701496726	756	29	11.6	562	13	BQ219227	AGENCOURT
684	29	11.6	474	14	CB729285	AMGNNUC:N	C 757	29	11.6	564	14	W26917	Human
C 685	29	11.6	474	14	CB729371	AMGNNUC:N	758	29	11.6	566	14	CB616634	AMGNNUC:U
C 686	29	11.6	474	28	AQ865712	nbeb0026G	759	29	11.6	567	13	BU851033	AGENCOURT
C 687	29	11.6	475	14	CB729042	AMGNNUC:M	760	29	11.6	567	14	CB616361	AMGNNUC:U
C 688	29	11.6	476	13	BQ949365	AGENCOURT	C 761	29	11.6	568	14	CB616179	AMGNNUC:N
689	29	11.6	476	14	CB732230	AMGNNUC:M	C 762	29	11.6	571	14	CB615495	AMGNNUC:N
690	29	11.6	477	14	CB315243	AGENCOURT	763	29	11.6	573	14	CB615030	AMGNNUC:S
C 691	29	11.6	478	14	CB731253	AMGNNUC:N	C 764	29	11.6	574	13	BU184818	AGENCOURT
C 692	29	11.6	479	13	BU535379	AMGNNUC:S	C 765	29	11.6	574	14	CB608371	AMGNNUC:U
693	29	11.6	479	14	CB7330896	AMGNNUC:S	766	29	11.6	578	13	BU442332	604145115
694	29	11.6	481	14	CB728525	AMGNNUC:N	767	29	11.6	582	12	BM074696	MEST296-D
695	29	11.6	483	12	BM340423	MEST322-E	C 768	29	11.6	582	13	BU562416	AGENCOURT
696	29	11.6	487	12	BM267465	BM267465 MEST367-B	769	29	11.6	583	12	BM350537	MEST267-R
697	29	11.6	487	13	BU589548	AGENCOURT	770	29	11.6	584	12	BM336112	MEST187-F
698	29	11.6	487	14	CB726623	AMGNNUC:S	771	29	11.6	584	14	CB586256	AMGNNUC:N
699	29	11.6	487	14	H15553	H15553 ym27e05.s1	772	29	11.6	585	11	AY112046	Zea mays
700	29	11.6	488	14	CB726240	AMGNNUC:U	773	29	11.6	585	12	BM267894	MEST373-F
701	29	11.6	491	9	AI996767	AI996767 701668292	C 774	29	11.6	585	14	CB585867	AMGNNUC:N
702	29	11.6	492	13	BU406049	BU406049 604137705	C 775	29	11.6	589	14	CB583383	AMGNNUC:C
703	29	11.6	492	14	CB546940	AMGNNUC:N	776	29	11.6	596	14	CB583943	AMGNNUC:N
C 704	29	11.6	493	14	CB713646	AMGNNUC:N	C 777	29	11.6	597	14	CB5833045	AMGNNUC:S
C 705	29	11.6	494	14	CB713438	AMGNNUC:N	C 778	29	11.6	598	14	CB582992	AMGNNUC:C
706	29	11.6	495	13	BU554578	BU554578 AGENCOURT	C 779	29	11.6	599	11	AY112262	Zea mays
707	29	11.6	495	13	BU595930	BU595930 AGENCOURT	780	29	11.6	604	13	BU961396	AGENCOURT
708	29	11.6	499	11	AY110677	AY110677 Zea mays	C 781	29	11.6	608	13	BU937469	AGENCOURT
C 709	29	11.6	500	13	BU867420	BU867420 S073A12_P	C 782	29	11.6	610	14	CB580562	AMGNNUC:N
710	29	11.6	501	9	AA495551	AA495551 c216 Zhou	C 783	29	11.6	610	14	CB580141	AMGNNUC:U
C 711	29	11.6	502	29	AG016501	AG016501 Homo sapi	C 784	29	11.6	612	9	AI996278	AI996278 701550984
712	29	11.6	503	13	BU345955	BU345955 604169149	C 785	29	11.6	612	14	CB580228	AMGNNUC:N
C 713	29	11.6	503	14	CA455726	CA455726 AGENCOURT	786	29	11.6	612	28	AZ197900	SP_1035_B
C 714	29	11.6	507	11	AY111917	AY111917 Zea mays	C 787	29	11.6	613	13	BU540219	AGENCOURT
C 715	29	11.6	507	29	AG016491	AG016491 Homo sapi	C 788	29	11.6	613	14	CB580141	AMGNNUC:U
C 716	29	11.6	507	29	AL756318	AL756318 Arabidops	C 789	29	11.6	614	14	CB579876	AMGNNUC:C
717	29	11.6	511	9	AW004331	AW004331 701956478	790	29	11.6	616	11	AY110283	Zea mays
718	29	11.6	513	12	BM332107	BM332107 MEST152-E	C 791	29	11.6	618	14	CB579172	AMGNNUC:U
C 719	29	11.6	513	13	BU954499	BU954499 AGENCOURT	792	29	11.6	619	13	BU440391	604147386
C 720	29	11.6	514	13	BU934633	BU934633 AGENCOURT	C 793	29	11.6	622	14	CB578549	AMGNNUC:N
C 721	29	11.6	515	13	BU174669	BU174669 AGENCOURT	794	29	11.6	622	14	CB578555	AMGNNUC:N
C 722	29	11.6	516	13	BQ689879	BQ689879 AGENCOURT	C 795	29	11.6	623	11	AY111379	Zea mays
723	29	11.6	516	14	CB716289	CB716289 AMGNNUC:U	C 796	29	11.6	624	29	AG016643	Homo sapi
C 724	29	11.6	517	12	BM349215	BM349215 MEST310-E	797	29	11.6	626	13	BU489428	604128147
725	29	11.6	517	14	CB716237	CB716237 AMGNNUC:N	C 798	29	11.6	629	14	CB577605	AMGNNUC:C
726	29	11.6	518	13	BU954054	BU954054 AGENCOURT	C 799	29	11.6	631	29	AG016896	Homo sapi
727	29	11.6	518	14	CB715949	CB715949 AMGNNUC:N	C 800	29	11.6	632	13	BU206678	604152015
C 728	29	11.6	519	13	BU533784	BU533784 AGENCOURT	801	29	11.6	633	11	AY111893	Zea mays
C 729	29	11.6	519	14	CA463709	CA463709 AGENCOURT	C 802	29	11.6	634	11	AY111941	Zea mays
730	29	11.6	521	12	BG810075	BG810075 mgct002x1	C 803	29	11.6	634	29	AG018510	Homo sapi
C 731	29	11.6	525	13	BU955334	BU955334 AGENCOURT	C 804	29	11.6	635	29	AG016630	Homo sapi
C 732	29	11.6	526	11	AY111350	AY111350 Zea mays	C 805	29	11.6	637	12	BM923996	AGENCOURT
C 733	29	11.6	527	13	BU600985	BU600985 AGENCOURT	C 806	29	11.6	642	13	BU401099	604136701
C 734	29	11.6	527	14	CB719821	CB719821 AMGNNUC:C	C 807	29	11.6	644	13	BU437841	604144523

C 808	29	11.6	644	29	CC312724	CC312724 TAM32-22F	C 881	29	11.6	781	13	BU956127	BU956127 AGENCOURT
C 809	29	11.6	645	13	BU848954	BU848954 AGENCOURT	882	29	11.6	786	28	AZ186079	AZ186079 SP_1006_A
C 810	29	11.6	645	29	AG018532	AG018532 Homo sapi	883	29	11.6	786	28	AZ196321	AZ196321 SP_1031_B
C 811	29	11.6	647	11	AY109954	AY109954 Zea mays	C 884	29	11.6	790	13	BU929666	BU929666 AGENCOURT
C 812	29	11.6	647	13	BU601487	BU601487 AGENCOURT	885	29	11.6	793	14	CD494711	CD494711 CDA12-D01
C 813	29	11.6	649	12	BM336743	BM336743 MEST198-C	C 886	29	11.6	794	13	BU860855	BU860855 AGENCOURT
C 814	29	11.6	649	13	BU558347	BU558347 AGENCOURT	C 887	29	11.6	794	14	CA464679	CA464679 AGENCOURT
C 815	29	11.6	651	14	CB557716	CB557716 AMGNNUC:C	888	29	11.6	797	14	CB781521	CB781521 AMGNNUC:N
C 816	29	11.6	653	29	AG017573	AG017573 Homo sapi	889	29	11.6	797	28	AQ749450	AQ749450 HS_5574_A
C 817	29	11.6	655	29	AG018576	AG018576 Homo sapi	C 890	29	11.6	799	13	BU937087	BU937087 AGENCOURT
C 818	29	11.6	656	11	AY111626	AY111626 Zea mays	C 891	29	11.6	802	28	BZ036009	BZ036009 oef84c06..
C 819	29	11.6	656	12	BM478204	BM478204 AGENCOURT	892	29	11.6	804	11	AY110971	AY110971 Zea mays
C 820	29	11.6	656	13	BQ435823	BQ435823 AGENCOURT	893	29	11.6	804	14	CB229945	CB229945 AGENCOURT
C 821	29	11.6	657	14	CB557423	CB557423 AMGNNUC:U	C 894	29	11.6	805	14	CA463139	CA463139 AGENCOURT
C 822	29	11.6	659	12	BM545980	BM545980 AGENCOURT	C 895	29	11.6	809	13	BU567626	BU567626 AGENCOURT
C 823	29	11.6	661	29	AG018552	AG018552 Homo sapi	896	29	11.6	812	14	CB314240	CB314240 AGENCOURT
C 824	29	11.6	663	13	BQ409297	BQ409297 GA_Ed001	C 897	29	11.6	813	13	BU841960	BU841960 AGENCOURT
C 825	29	11.6	663	29	AG017631	AG017631 Homo sapi	C 898	29	11.6	813	28	AZ133545	AZ133545 OSJNBb010
C 826	29	11.6	664	28	BH988217	BH988217 oeh29a01.	C 899	29	11.6	815	28	AZ187345	AZ187345 SP_1008_B
C 827	29	11.6	669	29	AG014898	AG014898 Homo sapi	C 900	29	11.6	824	13	BU599603	BU599603 AGENCOURT
C 828	29	11.6	671	11	AY110700	AY110700 Zea mays	901	29	11.6	827	10	BE053823	BE053823 GA_Ea003
C 829	29	11.6	672	28	BH955736	BH955736 odi48g07.	C 902	29	11.6	829	13	BU602111	BU602111 AGENCOURT
C 830	29	11.6	673	29	CC252330	CC252330 CH261-15M	C 903	29	11.6	832	13	BQ691470	BQ691470 AGENCOURT
C 831	29	11.6	673	29	AG017609	AG017609 Homo sapi	C 904	29	11.6	836	13	BU601403	BU601403 AGENCOURT
C 832	29	11.6	676	9	AI910355	AI910355 IL-BT226-	905	29	11.6	837	28	AQ745358	AQ745358 HS_2276_A
C 833	29	11.6	679	13	BU601923	BU601923 AGENCOURT	C 906	29	11.6	839	13	BU602213	BU602213 AGENCOURT
C 834	29	11.6	680	10	BG440852	BG440852 GA_Ea001	C 907	29	11.6	845	13	BQ673897	BQ673897 AGENCOURT
C 835	29	11.6	683	14	CB556679	CB556679 AMGNNUC:N	908	29	11.6	848	14	CB781513	CB781513 AMGNNUC:N
C 836	29	11.6	685	29	AG018069	AG018069 Homo sapi	909	29	11.6	849	29	AG120762	AG120762 Pan trogl
C 837	29	11.6	686	14	CB556629	CB556629 AMGNNUC:U	910	29	11.6	852	28	BH795465	BH795465 10D07LLJ0
C 838	29	11.6	690	29	AG018367	AG018367 Homo sapi	911	29	11.6	854	29	AG015766	AG015766 Homo sapi
C 839	29	11.6	692	13	BU506076	BU506076 AGENCOURT	C 912	29	11.6	857	29	CNS01809	AL108723 Drosophil
C 840	29	11.6	696	28	AQ273276	AQ273276 nbxb0029L	913	29	11.6	861	14	CB781503	CB781503 AMGNNUC:N
C 841	29	11.6	696	28	BH927182	BH927182 odi62e03.	C 914	29	11.6	863	14	CA464715	CA464715 AGENCOURT
C 842	29	11.6	698	13	BQ223373	BQ223373 AGENCOURT	C 915	29	11.6	864	13	BU189870	BU189870 AGENCOURT
C 843	29	11.6	700	13	BQ228631	BQ228631 AGENCOURT	C 916	29	11.6	865	11	AY109545	AY109545 Zea mays
C 844	29	11.6	702	28	AZ200795	AZ200795 SP_1011_A	917	29	11.6	869	11	AY110399	AY110399 Zea mays
C 845	29	11.6	704	12	BI887516	BI887516 ZF637-1-0	C 918	29	11.6	869	12	BM459157	BM459157 AGENCOURT
C 846	29	11.6	707	29	AG008864	AG008864 Homo sapi	919	29	11.6	873	13	BU554253	BU554253 AGENCOURT
C 847	29	11.6	715	12	BM465624	BM465624 AGENCOURT	C 920	29	11.6	874	13	BQ439047	BQ439047 AGENCOURT
C 848	29	11.6	715	29	AG016289	AG016289 Homo sapi	C 921	29	11.6	878	13	BQ670027	BQ670027 AGENCOURT
C 849	29	11.6	718	13	BQ276397	BQ276397 AGENCOURT	C 922	29	11.6	878	28	AZ192913	AZ192913 SP_1022_B
C 850	29	11.6	718	13	BU436218	BU436218 604145275	C 923	29	11.6	879	12	BI887897	BI887897 ZF637-1-0
C 851	29	11.6	722	11	AY111372	AY111372 Zea mays	C 924	29	11.6	879	13	BE000832	BE000832 AGENCOURT
C 852	29	11.6	722	11	AY112175	AY112175 Zea mays	C 925	29	11.6	881	10	BE035058	BE035058 MM02C11_M
C 853	29	11.6	722	28	BH971184	BH971184 odi80a01.	926	29	11.6	885	13	BU843837	BU843837 AGENCOURT
C 854	29	11.6	722	29	AG016309	AG016309 Homo sapi	C 927	29	11.6	886	14	CB314376	CB314376 AGENCOURT
C 855	29	11.6	723	13	BU529127	BU529127 AGENCOURT	928	29	11.6	888	11	AY110623	AY110623 Zea mays
C 856	29	11.6	724	28	AZ192045	AZ192045 SP_1020_B	C 929	29	11.6	888	13	BU521349	BU521349 AGENCOURT
C 857	29	11.6	727	11	AY111186	AY111186 Zea mays	C 930	29	11.6	889	13	BQ952397	BQ952397 AGENCOURT
C 858	29	11.6	731	13	BU516803	BU516803 AGENCOURT	931	29	11.6	890	14	CA988355	CA988355 AGENCOURT
C 859	29	11.6	733	13	BJ942273	BU942273 AGENCOURT	C 932	29	11.6	893	13	BU160416	BU160416 AGENCOURT
C 860	29	11.6	733	29	AG001939	AG001939 Homo sapi	C 933	29	11.6	895	13	BQ430170	BQ430170 AGENCOURT
C 861	29	11.6	738	13	BU196177	BU196177 AGENCOURT	C 934	29	11.6	899	14	CB781493	CB781493 AMGNNUC:N
C 862	29	11.6	741	29	AG018391	AG018391 Homo sapi	935	29	11.6	900	28	AZ174701	AZ174701 SP_0130_A
C 863	29	11.6	742	28	BH988696	BH988696 oeh18g02.	C 936	29	11.6	901	13	BU963564	BU963564 AGENCOURT
C 864	29	11.6	743	13	BU563781	BU563781 AGENCOURT	C 937	29	11.6	902	13	BU842217	BU842217 AGENCOURT
C 865	29	11.6	744	14	CA455561	CA455561 AGENCOURT	C 938	29	11.6	902	13	BX409664	BX409664
C 866	29	11.6	746	12	BM267558	BM267558 MEST368-D	C 939	29	11.6	906	13	BU164521	BU164521 AGENCOURT
C 867	29	11.6	748	12	BI889086	BI889086 ZF637-2-0	C 940	29	11.6	908	28	AQ739004	AQ739004 HS_5384_B
C 868	29	11.6	748	12	BI892168	BI892168 ZF637-3-0	941	29	11.6	909	11	AY111054	AY111054 Zea mays
C 869	29	11.6	750	28	BH997260	BH997260 oef68d08.	942	29	11.6	911	13	BU961153	BU961153 AGENCOURT
C 870	29	11.6	756	13	BQ927229	BQ927229 AGENCOURT	C 943	29	11.6	913	14	CA494505	CA494505 AGENCOURT
C 871	29	11.6	757	13	BU961245	BU961245 AGENCOURT	944	29	11.6	915	13	BU798845	BU798845 SJF2BHB06
C 872	29	11.6	759	12	BM341661	BM341661 MEST337-G	945	29	11.6	918	14	CA455626	CA455626 AGENCOURT
C 873	29	11.6	760	28	BH995646	BH995646 oef83a02.	C 946	29	11.6	921	14	CA794081	CA794081 AGENCOURT
C 874	29	11.6	761	13	BU954442	BU954442 AGENCOURT	947	29	11.6	925	13	BX409887	BX409887
C 875	29	11.6	767	13	BU857064	BU857064 AGENCOURT	948	29	11.6	929	13	BU164541	BU164541 AGENCOURT
C 876	29	11.6	770	13	BU599993	BU599993 AGENCOURT	C 949	29	11.6	933	14	CA988761	CA988761 AGENCOURT
C 877	29	11.6	772	12	BM544455	BM544455 AGENCOURT	C 950	29	11.6	949	11	AY112250	AY112250 Zea mays
C 878	29	11.6	772	29	CC317576	CC317576 TAM32-3F6	C 951	29	11.6	953	14	CA986448	CA986448 AGENCOURT
C 879	29	11.6	779	14	CB208006	CB208006 AGENCOURT	952	29	11.6	955	14	CA471305	CA471305 AGENCOURT
C 880	29	11.6	780	11	AY111086	AY111086 Zea mays	C 953	29	11.6	957	13	BQ949643	BQ949643 AGENCOURT



c 954	29	11.6	957	14	CD325113	CD325113	AGENCOURT
c 955	29	11.6	958	14	CB181369	CB181369	AGENCOURT
c 956	29	11.6	967	11	AY109993	AY109993	Zea mays
c 957	29	11.6	967	13	BX431737	BX431737	
c 958	29	11.6	968	29	AG080780	AG080780	Pan trogl
c 959	29	11.6	972	13	BU944399	BU944399	AGENCOURT
c 960	29	11.6	974	13	BQ926652	BQ926652	AGENCOURT
c 961	29	11.6	990	13	BU944424	BU944424	AGENCOURT
c 962	29	11.6	995	13	BX374301	BX374301	
c 963	29	11.6	1000	29	CC253524	CC253524	CH261-115
c 964	29	11.6	1003	11	AY109801	AY109801	Zea mays
c 965	29	11.6	1003	13	BU591355	BU591355	AGENCOURT
c 966	29	11.6	1005	29	CC233173	CC233173	CH261-87J
c 967	29	11.6	1010	13	BX450807	BX450807	
c 968	29	11.6	1013	14	CB562727	CB562727	AGENCOURT
c 969	29	11.6	1017	13	BU931691	BU931691	AGENCOURT
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c 973	29	11.6	1033	13	BX330627	BX330627	
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c 975	29	11.6	1045	12	BM808518	BM808518	AGENCOURT
c 976	29	11.6	1048	14	CB320738	CB320738	AGENCOURT
c 977	29	11.6	1054	10	BE422421	BE422421	HWM024CF
c 978	29	11.6	1055	13	BU961525	BU961525	AGENCOURT
c 979	29	11.6	1056	29	CC215744	CC215744	CH261-189
c 980	29	11.6	1058	11	AY109910	AY109910	Zea mays
c 981	29	11.6	1061	11	AY110008	AY110008	Zea mays
c 982	29	11.6	1061	14	CB605930	CB605930	AMGNUUC:N
c 983	29	11.6	1067	29	CC275375	CC275375	CH261-76G
c 984	29	11.6	1078	14	CB203689	CB203689	AGENCOURT
c 985	29	11.6	1079	14	CB202455	CB202455	AGENCOURT
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c 987	29	11.6	1085	12	BM547657	BM547657	AGENCOURT
c 988	29	11.6	1087	29	CC224160	CC224160	CH261-114
c 989	29	11.6	1094	12	BM462958	BM462958	AGENCOURT
c 990	29	11.6	1114	11	AY112169	AY112169	Zea mays
c 991	29	11.6	1126	12	BM454022	BM454022	AGENCOURT
c 992	29	11.6	1127	14	CD507381	CD507381	CDA84-G02
c 993	29	11.6	1128	12	BQ061453	BQ061453	AGENCOURT
c 994	29	11.6	1129	12	BQ058425	BQ058425	AGENCOURT
c 995	29	11.6	1139	10	BE034978	BE034978	MN01A01 M
c 996	29	11.6	1155	29	CC214553	CC214553	CH261-116
c 997	29	11.6	1164	29	CC261365	CC261365	CH261-72H
c 998	29	11.6	1165	13	BU526465	BU526465	AGENCOURT
c 999	29	11.6	1168	14	CD500341	CD500341	CDA44-E03
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ALIGNMENTS

RESULT 1  
BU764411 218 bp mRNA linear EST 10-OCT-2002  
LOCUS sas01a10.y2 Gm-cl080 Glycine max cDNA clone SOYBEAN CLONE ID:  
DEFINITION Gm-cl080-2347 5' similar to TR:Q9SW25 Q9SW25 MTN3-LIKE PROTEIN. ; mRNA sequence.

ACCESSION BU764411  
VERSION BU764411.1 GI:23732505  
KEYWORDS EST.

SOURCE Glycine max (soybean)  
ORGANISM Glycine max

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids ; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.

REFERENCE 1 (bases 1 to 218)  
AUTHORS Shoemaker,R., Keim,P., Vodkin,L., Erpelding,J., Coryell,V., Khanna ,A., Bolla,B., Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers ,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk ,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann

TITLE  
JOURNAL  
COMMENT  
R., Waterston,R. and Wilson,R.  
Public Soybean EST Project  
Unpublished  
Contact: Shoemaker R/Public Soybean EST Project  
Public Soybean EST Project  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: est@watson.wustl.edu  
This clone is available through: ResGen, Invitrogen Corp. 2130 South Memorial Parkway Huntsville, AL 35801 For further information call: (800)-533-4363 or contact: ccu@resgen.com web site: www.resgen.com  
Seq primer: -40RP from Gibco  
High quality sequence stop: 128.  
Location/Qualifiers  
1. .218  
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/tissue\_type="Roots of 8 day old 'Bragg' supernodulating mutant N7S382 seedlings"  
/dev\_stage="8 days old"  
/lab\_host="DH10B"  
/clone\_lib="Gm-cl080"  
/note="Vector: pBluescript II SK+; Site 1: EcoRI; Site 2: XhoI; The mRNA was isolated from roots of 8 day old 'Bragg' supernodulating mutant NTS382 seedlings that were infected with Bradyrhizobium japonicum, strain USDA 110, 72 hours prior to harvest. Dr. Gary Stacey generously donated the tissue. The roots were flash-frozen in liquid nitrogen. Stratagene's cDNA Synthesis Kit (catalog number 200401) was used to synthesize the cDNA. First-strand synthesis was performed with 5-methyl dCTP, hence the ligated cDNA was hemimethylated. A modification of Stratagene's first-strand synthesis primer was used. An 'anchor' nucleotide (V=A, C, or G) was added to the 3' end of the primer [GAGAGAGAGAGAGAGAGACTAGTCTCGAG(T)18V] to anchor the primer at the 5' end of the poly(A) tract. After second-strand synthesis, the cDNA ends were filled in with cloned Pfu DNA, ligated to EcoRI adapters and subsequently phosphorylated. The cDNA was then precipitated and redissolved in sterile, RNase-, DNase-free water. The XhoI site within the first- strand synthesis primer was then restricted by digestion with XhoI from Promega (40U/ul); all XhoI sites in the cDNA would be protected by their hemimethylated status. The cDNA constructs were size-fractionated with a 500bp cutoff, using Sephacryl S-500 High Resolution (Pharmacia Biotech) in a 2-mm diameter column and a bed volume of approximately 1ml. The column eluent was precipitated, redissolved, and ligated into Stratagene's pBluescript II XR Predigested vector (pBluescript II SK(+)) vector that has been digested with EcoRI and XhoI, and phosphorylated by Stratagene). This library was constructed in the laboratory of Dr. Paul Keim and Dr. Virginia H. Coryell at Northern Arizona University."

BASE COUNT 60 a 50 c 39 g 69 t  
ORIGIN  
Query Match 46.2%; Score 116; DB 13; Length 218;  
Best Local Similarity 100.0%; Pred. No. 2.9e-50;  
Matches 116; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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|||||  
Db 101 TTCCAAAACCATGTCCACAGTCATCTAAGTTTCGCCCTTTGGGATTTAGGTAACATTGC 160  
QY 185 CTCCTTCGTGTGCTTTCTGGCACCACCTACCAACATTTATAGAGTTTGTGAAGAAGA 240  
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Db 161 CTCCTTCGTGTGCTTTCTGGCACCACCTACCAACATTTATAGAGTTTGTGAAGAAGA 216



RESULT 2  
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OCUS  
DEFINITION  
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Gm-cl054-845 5' similar to TR:P93332 P93332 MTN3 GENE PRECURSOR. ; ,  
mRNA sequence.  
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BF068522  
EST.  
BF068522.1 GI:10645385  
EYWORDS  
Glycine max (soybean)  
SOURCE  
ORGANISM  
Glycine max  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids  
; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;  
Glycine.  
REFERENCE  
1 (bases 1 to 389)  
AUTHORS  
Shoemaker,R., Keim,P., Vodkin,L., Erpelding,J., Coryell,V., Khanna  
,A., Bolla,B., Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C.,  
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,R., Ritter,B., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann  
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Unpublished  
Contact: Shoemaker R/Public Soybean EST Project  
Public Soybean EST Project  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: est@watson.wustl.edu  
This clone is available through: ResGen, Invitrogen Corp. 2130  
South Memorial Parkway Huntsville, AL 35801 For further information  
call: (800)-533-4363 or contact via email: ccu@resgen.com  
Insert length: 1390 Std Error: 0.00  
High quality sequence stop: 346.  
Location/Qualifiers  
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/lab\_host="DH10B"  
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/note="Vector: pBluescript II SK+; Site 1: EcoRI; Site 2:  
XhoI; The Harosoy NIL was constructed and seed was  
provided by Dr. J. Specht, University of Nebraska  
(Shoemaker and Specht, 1995). The cDNA library was  
constructed from mRNA isolated from leaf tissue at various  
developmental stages of 3 week old greenhouse grown  
plants. Complementary DNA was synthesized from mRNA using  
a primer consisting of a poly(dT) sequence with a XhoI  
restriction site and a 3' anchor. EcoRI adapters were  
ligated to the blunt-ended cDNA fragments followed by  
XhoI digestion. The cDNA fragments were directionally  
cloned into the EcoRI-XhoI restriction site of the  
pBluescript vector. The ligated cDNA fragments were  
transformed into DH10B host cells (GibcoBRL). This  
library was constructed in cooperation with Dr. Paul  
Keim's laboratory at Northern Arizona University."

FEATURES

source

ASE COUNT 106 a 89 c 73 g 120 t 1 others  
RIGIN  
Query Match 46.2%; Score 116; DB 10; Length 389;  
Best Local Similarity 100.0%; Pred. No. 3.3e-50;  
Matches 116; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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b 110 TTCAAAACCATGTCCACAGTCATCTAAGTTTCGCCTTTGGGATTCTAGGTAACATTGC 169

QY 185 CTCCTTCGTGTGCTTTCTGGCACCACACTACCAACATTTTATAGAGTTTGTAAAGA 240  
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Db 170 CTCCTTCGTGTGCTTTCTGGCACCACACTACCAACATTTTATAGAGTTTGTAAAGA 225  
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LOCUS  
DEFINITION  
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su09e10.y1 Gm-cl066 Glycine max cDNA clone GENOME SYSTEMS CLONE ID:  
Gm-cl066-1004 5' similar to TR:O82587 O82587 MTN3 HOMOLOG. ; , mRNA  
sequence.  
ACCESSION  
BU090931  
VERSION  
BU090931.1 GI:22541088  
KEYWORDS  
EST.  
SOURCE  
Glycine max (soybean)  
ORGANISM  
Glycine max  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids  
; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;  
Glycine.  
REFERENCE  
1 (bases 1 to 450)  
AUTHORS  
Shoemaker,R., Keim,P., Vodkin,L., Erpelding,J., Coryell,V., Khanna  
,A., Bolla,B., Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C.,  
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Contact: Shoemaker R/Public Soybean EST Project  
Public Soybean EST Project  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: est@watson.wustl.edu  
This clone is available through: Genome Systems, Inc. 4633 World  
Parkway Circle St. Louis, Missouri 63134 For further information  
call: (800) 430-0030 or (314) 427-3222 FAX: (888) 919-3324 or (314)  
427-3324 or contact: clones@genomesystems.com or  
info@genomesystems.com web site: www.genomesystems.com  
High quality sequence stop: 424.  
Location/Qualifiers  
1. .450  
/organism="Glycine max"  
/mol\_type="mRNA"  
/db\_xref="taxon:3847"  
/clone="GENOME SYSTEMS CLONE ID: Gm-cl066-1004"  
/tissue\_type="Leaf and shoot tip, salt stressed, 2 week  
old seedling"  
/lab\_host="DH10B"  
/clone\_lib="Gm-cl066"  
/note="Vector: pBluescript II SK+; Site 1: EcoRI; Site 2:  
XhoI; The cDNA library was constructed from mRNA isolated  
from unexpanded leaves and the shoot tips of 2 week old  
seedlings from the cultivar Williams. The 2 week old  
seedlings were salt stressed in a solution of 500mM NaCl  
for 3 days prior to harvesting. Complementary DNA was  
synthesized from mRNA using a primer consisting of a  
poly(dT) sequence with a XhoI restriction site. EcoRI  
adapters were ligated to the blunt-ended cDNA fragments  
followed by XhoI digestion. The cDNA fragments were  
directionally cloned into the EcoRI-XhoI restriction site  
of the pBluescript vector. The ligated cDNA fragments were  
transformed into DH10B host cells (GibcoBRL). This library  
was constructed in the laboratory of Dr. Randy  
Shoemaker."

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source

BASE COUNT 121 a 95 c 90 g 144 t  
ORIGIN  
Query Match 46.2%; Score 116; DB 13; Length 450;  
Best Local Similarity 100.0%; Pred. No. 3.3e-50;

Matches 116; Conservative 0; Mismatches 0; Indels 0; Gaps 0	
QY	125 TTCCAAAACCATGTCCACAGTCATCTAAGTTTCGCTTTGGGATTCTAGGTAACATTGC 184
db	108 TTCCAAAACCATGTCCACAGTCATCTAAGTTTCGCTTTGGGATTCTAGGTAACATTGC 167
QY	185 CTCCTTCGTGTGCTTTCTGGCACCACCTACCAACATTTTATAGAGTTTGTAAAGAAGA 240
db	168 CTCCTTCGTGTGCTTTCTGGCACCACCTACCAACATTTTATAGAGTTTGTAAAGAAGA 223
RESULT 4	
BG041196	
LOCUS	
DEFINITION	
Gm-cl057-1155 5' similar to TR:082587 082587 MTN3 HOMOLOG. ;, mRNA sequence.	
BG041196	
VERSION	
KEYWORDS	
SOURCE	
ORGANISM	
Glycine max (soybean)	
Glycine max	
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.	
1 (bases 1 to 457)	
REFERENCE	
AUTHORS	
Shoemaker,R., Keim,P., Vodkin,L., Erpelding,J., Coryell,V., Khanna,A., Bolla,B., Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wyllie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R. and Wilson,R.	
Public Soybean EST Project	
Unpublished	
Contact: Shoemaker R/Public Soybean EST Project	
Public Soybean EST Project	
Washington University School of Medicine	
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA	
Tel: 314 286 1800	
Fax: 314 286 1810	
Email: est@watson.wustl.edu	
This clone is available through: ResGen, Invitrogen Corp. 2130 South Memorial Parkway Huntsville, AL 35801 For further information: call: (800)-533-4363 or contact via email: ccu@resgen.com	
High quality sequence stop: 423.	
Location/Qualifiers	
1. .457	
/organism="Glycine max"	
/mol_type="mRNA"	
/db_xref="taxon:3847"	
/clone="GENOME SYSTEMS CLONE ID: Gm-cl057-1155"	
/tissue_type="Degenerating cotyledons, 2 week old seedling"	
/lab_host="DH10B"	
/clone_lib="Gm-cl057"	
/note="Vector: pBluescript II SK+; Site 1: EcoRI; Site 2: XhoI; The cDNA library was constructed from mRNA isolated from degenerating cotyledons of 2 week old seedlings from PI468916. Complementary DNA was synthesized from mRNA using a primer consisting of a poly(dT) sequence with a XhoI restriction site. EcoRI adapters were ligated to the blunt-ended cDNA fragments followed by XhoI digestion. The cDNA fragments were directionally cloned into the EcoRI-XhoI restriction site of the pBluescript vector. The ligated cDNA fragments were transformed into DH10B host cells (GibcoBRL). This library was constructed in the laboratory of Dr. Randy Shoemaker."	
ASE COUNT	126 a 96 c 92 g 143 t
RIGIN	
Query Match	46.2%; Score 116; DB 10; Length 457;
Best Local Similarity	100.0%; Pred. No. 3.4e-50;

Matches 116; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY	125 TTCCAAAACCATGTCCACAGTCATCTAAGTTTCGCTTTGGGATTCTAGGTAACATTGC 184
Ddb	115 TTCCAAAACCATGTCCACAGTCATCTAAGTTTCGCTTTGGGATTCTAGGTAACATTGC 174
QY	185 CTCCTTCGTGTGCTTTCTGGCACCACCTACCAACATTTTATAGAGTTTGTAAAGAAGA 240
Ddb	175 CTCCTTCGTGTGCTTTCTGGCACCACCTACCAACATTTTATAGAGTTTGTAAAGAAGA 230
RESULT 5	
BE804090	
LOCUS	
DEFINITION	
sr75f12.y1 Gm-cl052 Glycine max cDNA clone GENOME SYSTEMS CLONE ID: Gm-cl052-1608 5' similar to TR:082587 082587 MTN3 HOMOLOG. ;, mRNA sequence.	
BE804090	
VERSION	
KEYWORDS	
SOURCE	
ORGANISM	
Glycine max (soybean)	
Glycine max	
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids ; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.	
1 (bases 1 to 473)	
REFERENCE	
AUTHORS	
Shoemaker,R., Keim,P., Vodkin,L., Erpelding,J., Coryell,V., Khanna ,A., Bolla,B., Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wyllie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers ,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk ,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann ,R., Waterston,R. and Wilson,R.	
Public Soybean EST Project	
Unpublished	
Contact: Shoemaker R/Public Soybean EST Project	
Public Soybean EST Project	
Washington University School of Medicine	
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA	
Tel: 314 286 1800	
Fax: 314 286 1810	
Email: est@watson.wustl.edu	
This clone is available through: ResGen, Invitrogen Corp. 2130 South Memorial Parkway Huntsville, AL 35801 For further information call: (800)-533-4363 or contact via email: ccu@resgen.com	
Insert Length: 1929 Std Error: 0.00	
High quality sequence stop: 404.	
Location/Qualifiers	
1. .473	
/organism="Glycine max"	
/mol_type="mRNA"	
/db_xref="taxon:3847"	
/clone="GENOME SYSTEMS CLONE ID: Gm-cl052-1608"	
/tissue_type="whole seedlings of greenhouse grown plants"	
/dev_stage="1 week old"	
/lab_host="DH10B"	
/clone_lib="Gm-cl052"	
/note="Vector: pBluescript II SK+; Site_1: EcoRI; Site_2: XhoI; The Harosoy NIL was constructed and seed was provided by Dr. J. Specht, University of Nebraska (Shoemaker and Specht, 1995). The cDNA library was constructed from mRNA isolated from whole seedlings of 1 week old greenhouse grown plants. Complementary DNA was synthesized from mRNA using a primer consisting of a poly(dT) sequence with a XhoI restriction site and a 3' anchor. EcoRI adapters were ligated to the blunt-ended cDNA fragments followed by XhoI digestion. The cDNA fragments were directionally cloned into the EcoRI-XhoI restriction site of the pBluescript vector. The ligated cDNA fragments were transformed into DH10B host cells (GibcoBRL). The library was constructed in cooperation with Dr. Paul Keim's laboratory at Northern Arizona University."	
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source	

ASE COUNT 127 a 103 c 99 g 144 t  
RIGIN

Query Match 46.2%; Score 116; DB 10; Length 473;  
Best Local Similarity 100.0%; Pred. No. 3.4e-50;  
Matches 116; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y 125 TTCCAAACCATGTCCACAGTCATCTAAGTTTCGCCTTTGGGATTTCTAGGTAACATTGC 184  
|||||  
b 116 TTCCAAACCATGTCCACAGTCATCTAAGTTTCGCCTTTGGGATTTCTAGGTAACATTGC 175  
|||||

Y 185 CTCCTTCGTGTGCTTTCTGGCACCACACTACCAACATTTTATAGAGTTTGTAAAGAAGA 240  
|||||  
b 176 CTCCTTCGTGTGCTTTCTGGCACCACACTACCAACATTTTATAGAGTTTGTAAAGAAGA 231  
|||||

ESULT 6  
M887247  
OCUS BM887247 531 bp mRNA linear EST 08-MAR-2002  
EFINITION sam36a12.y1 Gm-cl068 Glycine max cDNA clone SOYBEAN CLONE ID:  
Gm-cl068-6576 5' similar to TR:082587 082587 MTN3 HOMOLOG. ; , mRNA  
sequence.  
BM887247  
BM887247.1 GI:19270991  
EST.  
Glycine max (soybean)  
ORGANISM Glycine max  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids  
; eurosids 1; Fabales; Fabaceae; Papilionoideae; Phaseoleae;  
Glycine.  
1 (bases 1 to 531)  
Shoemaker,R., Keim,P., Vodkin,L., Erpelding,J., Coryell,V., Khanna  
,A., Bolla,B., Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C.,  
Wyllie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers  
,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk  
,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann  
,R., Waterston,R. and Wilson,R.  
Public Soybean EST Project  
Unpublished  
Contact: Shoemaker R/Public Soybean EST Project  
Public Soybean EST Project  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: est@watson.wustl.edu  
This clone is available through: ResGen, Invitrogen Corp. 2130  
South Memorial Parkway Huntsville, AL 35801 For further information  
call: (800)-533-4363 or contact: ccu@resgen.com web site:  
www.resgen.com

Seq primer: -40RP from Gibco  
High quality sequence stop: 432.  
Location/Qualifiers  
1. .531  
/organism="Glycine max"  
/mol\_type="mRNA"  
/db\_xref="taxon:3847"  
/clone="SOYBEAN CLONE ID: Gm-cl068-6576"  
/tissue\_type="Leaf, drought stressed, 1 month old plants,  
greenhouse grown"  
/lab\_host="DH10B"  
/clone\_lib="Gm-cl068"  
/note="Vector: pBluescript II SK+; Site 1: EcoRI; Site 2:  
XhoI; The cDNA library was constructed from mRNA isolated  
from drought stressed leaf tissue of the cultivar Williams  
82. The month old greenhouse grown plants were deprived of  
water for 3 days prior to harvesting the stressed leaf  
tissue. Complementary DNA was synthesized from mRNA using  
a primer consisting of a poly(dT) sequence with a XhoI  
restriction site. EcoRI adapters were ligated to the  
blunt-ended cDNA fragments followed by XhoI digestion. The  
cDNA fragments were directionally cloned into the

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EcoRI-XhoI restriction site of the pBluescript vector. The  
ligated cDNA fragments were transformed into DH10B host  
cells (GibcoBRL). This library was constructed in the  
laboratory of Dr. Randy Shoemaker."

BASE COUNT 141 a 116 c 108 g 166 t  
ORIGIN

Query Match 46.2%; Score 116; DB 12; Length 531;  
Best Local Similarity 100.0%; Pred. No. 3.5e-50;  
Matches 116; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 125 TTCCAAACCATGTCCACAGTCATCTAAGTTTCGCCTTTGGGATTTCTAGGTAACATTGC 184  
|||||  
Db 101 TTCCAAACCATGTCCACAGTCATCTAAGTTTCGCCTTTGGGATTTCTAGGTAACATTGC 160  
|||||

QY 185 CTCCTTCGTGTGCTTTCTGGCACCACACTACCAACATTTTATAGAGTTTGTAAAGAAGA 240  
|||||  
Db 161 CTCCTTCGTGTGCTTTCTGGCACCACACTACCAACATTTTATAGAGTTTGTAAAGAAGA 216  
|||||

RESULT 7  
BM891617 554 bp mRNA linear EST 11-MAR-2002  
LOCUS sam41g03.y1 Gm-cl068 Glycine max cDNA clone SOYBEAN CLONE ID:  
Gm-cl068-7589 5' similar to TR:082587 082587 MTN3 HOMOLOG. ; , mRNA  
sequence.  
BM891617  
BM891617.1 GI:19346737  
DEFINITION EST.  
Glycine max (soybean)  
ORGANISM Glycine max  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids  
; eurosids 1; Fabales; Fabaceae; Papilionoideae; Phaseoleae;  
Glycine.  
1 (bases 1 to 554)  
Shoemaker,R., Keim,P., Vodkin,L., Erpelding,J., Coryell,V., Khanna  
,A., Bolla,B., Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C.,  
Wyllie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers  
,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk  
,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann  
,R., Waterston,R. and Wilson,R.  
Public Soybean EST Project  
Unpublished  
Contact: Shoemaker R/Public Soybean EST Project  
Public Soybean EST Project  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: est@watson.wustl.edu  
This clone is available through: ResGen, Invitrogen Corp. 2130  
South Memorial Parkway Huntsville, AL 35801 For further information  
call: (800)-533-4363 or contact: ccu@resgen.com web site:  
www.resgen.com

Seq primer: -40RP from Gibco  
High quality sequence stop: 421.  
Location/Qualifiers  
1. .554  
/organism="Glycine max"  
/mol\_type="mRNA"  
/db\_xref="taxon:3847"  
/clone="SOYBEAN CLONE ID: Gm-cl068-7589"  
/tissue\_type="Leaf, drought stressed, 1 month old plants,  
greenhouse grown"  
/lab\_host="DH10B"  
/clone\_lib="Gm-cl068"  
/note="Vector: pBluescript II SK+; Site 1: EcoRI; Site 2:  
XhoI; The cDNA library was constructed from mRNA isolated  
from drought stressed leaf tissue of the cultivar Williams  
82. The month old greenhouse grown plants were deprived of  
water for 3 days prior to harvesting the stressed leaf  
tissue. Complementary DNA was synthesized from mRNA using

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a primer consisting of a poly(dT) sequence with a XhoI restriction site. EcoRI adapters were ligated to the blunt-ended cDNA fragments followed by XhoI digestion. The cDNA fragments were directionally cloned into the EcoRI-XhoI restriction site of the pBluescript vector. The ligated cDNA fragments were transformed into DH10B host cells (GibcoBRL). This library was constructed in the laboratory of Dr. Randy Shoemaker."

BASE COUNT 148 a 119 c 113 g 174 t  
ORIGIN

Query Match 46.2%; Score 116; DB 12; Length 554;  
Best Local Similarity 100.0%; Pred. No. 3.5e-50;  
Matches 116; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 125 TTCCAAAACCAAGTCCACAGTCATCTAAGTTTCGCCCTTTGGGATTCTAGGTAACATTGC 184  
|||||  
DB 113 TTCCAAAACCAAGTCCACAGTCATCTAAGTTTCGCCCTTTGGGATTCTAGGTAACATTGC 172  
|||||  
QY 185 CTCCTTCGTGTGCTTCTGGCACCACCTACCAACATTTTATAGAGTTTGTAAAGAAGA 240  
|||||  
DB 173 CTCCTTCGTGTGCTTCTGGCACCACCTACCAACATTTTATAGAGTTTGTAAAGAAGA 228  
|||||

RESULT 8  
BM093555  
LOCUS  
DEFINITION  
ID: Gm-cl066-2517 5' similar to TR:082587 O82587 MTN3 HOMOLOG. ;  
mRNA sequence.

ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
Glycine max (soybean)  
Glycine max  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids  
; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;  
Glycine.

REFERENCE  
AUTHORS  
1 (bases 1 to 575)  
Shoemaker,R., Keim,P., Vodkin,L., Erpelding,J., Coryell,V., Khanna  
,A., Bolla,B., Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C.,  
Wyllie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers  
,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk  
,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann  
,R., Waterston,R. and Wilson,R.  
Public Soybean EST Project  
Unpublished

TITLE  
JOURNAL  
COMMENT  
Contact: Shoemaker R/Public Soybean EST Project  
Public Soybean EST Project  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: est@watson.wustl.edu  
This clone is available through: ResGen, Invitrogen Corp. 2130  
South Memorial Parkway Huntsville, AL 35801 For further information  
call: (800)-533-4363 or contact via email: ccu@resgen.com  
High quality sequence stop: 421.  
Location/Qualifiers  
1. .575  
/organism="Glycine max"  
/mol\_type="mRNA"  
/db\_xref="taxon:3847"  
/clone="GENOME SYSTEMS CLONE ID: Gm-cl066-2517"  
/tissue\_type="Leaf and shoot tip, salt stressed, 2 week  
old seedling"  
/lab\_host="DH10B"  
/clone\_lib="Gm-cl066"  
/note="Vector: pBluescript II SK+; Site 1: EcoRI; Site 2:  
XhoI; The cDNA library was constructed from mRNA isolated  
from unexpanded leaves and the shoot tips of 2 week old  
seedling from the cultivar Williams. The 2 week old

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seedlings were salt stressed in a solution of 500mM NaCl for 3 days prior to harvesting. Complementary DNA was synthesized from mRNA using a primer consisting of a poly(dT) sequence with a XhoI restriction site. EcoRI adapters were ligated to the blunt-ended cDNA fragments followed by XhoI digestion. The cDNA fragments were directionally cloned into the EcoRI-XhoI restriction site of the pBluescript vector. The ligated cDNA fragments were transformed into DH10B host cells (GibcoBRL). This library was constructed in the laboratory of Dr. Randy Shoemaker."

BASE COUNT 154 a 124 c 116 g 181 t  
ORIGIN

Query Match 46.2%; Score 116; DB 12; Length 575;  
Best Local Similarity 100.0%; Pred. No. 3.5e-50;  
Matches 116; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 125 TTCCAAAACCAAGTCCACAGTCATCTAAGTTTCGCCCTTTGGGATTCTAGGTAACATTGC 184  
|||||  
DB 113 TTCCAAAACCAAGTCCACAGTCATCTAAGTTTCGCCCTTTGGGATTCTAGGTAACATTGC 172  
|||||  
QY 185 CTCCTTCGTGTGCTTCTGGCACCACCTACCAACATTTTATAGAGTTTGTAAAGAAGA 240  
|||||  
DB 173 CTCCTTCGTGTGCTTCTGGCACCACCTACCAACATTTTATAGAGTTTGTAAAGAAGA 228  
|||||

RESULT 9  
BM886347  
LOCUS  
DEFINITION  
ID: Gm-cl068-4799 5' similar to TR:082587 O82587 MTN3 HOMOLOG. ;  
mRNA sequence.

ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
Glycine max (soybean)  
Glycine max  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids  
; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;  
Glycine.

REFERENCE  
AUTHORS  
1 (bases 1 to 578)  
Shoemaker,R., Keim,P., Vodkin,L., Erpelding,J., Coryell,V., Khanna  
,A., Bolla,B., Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C.,  
Wyllie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers  
,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk  
,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann  
,R., Waterston,R. and Wilson,R.  
Public Soybean EST Project  
Unpublished

TITLE  
JOURNAL  
COMMENT  
Contact: Shoemaker R/Public Soybean EST Project  
Public Soybean EST Project  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: est@watson.wustl.edu  
This clone is available through: ResGen, Invitrogen Corp. 2130  
South Memorial Parkway Huntsville, AL 35801 For further information  
call: (800)-533-4363 or contact: ccu@resgen.com web site:  
www.resgen.com  
Seq primer: -40RP from Gibco  
High quality sequence stop: 430.  
Location/Qualifiers  
1. .578  
/organism="Glycine max"  
/mol\_type="mRNA"  
/db\_xref="taxon:3847"  
/clone="SOYBEAN CLONE ID: Gm-cl068-4799"  
/tissue\_type="Leaf, drought stressed, 1 month old plants,  
greenhouse grown"  
/lab\_host="DH10B"

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AUTHORS Shoemaker,R., Keim,P., Vodkin,L., Erpelding,J., Coryell,V., Khanna ,A., Bolla,B., Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers ,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk ,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann ,R., Waterston,R. and Wilson,R.  
TITLE Public Soybean EST Project  
JOURNAL Unpublished  
COMMENT Contact: Shoemaker R/Public Soybean EST Project  
Public Soybean EST Project  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: est@watson.wustl.edu  
This clone is available through: ResGen, Invitrogen Corp. 2130 South Memorial Parkway Huntsville, AL 35801 For further information call: (800)-533-4363 or contact via email: ccu@resgen.com  
Seq primer: -40RP from Gibco  
High quality sequence stop: 444.  
Location/Qualifiers  
1. .565  
/organism="Glycine max"  
/mol\_type="mRNA"  
/db\_xref="taxon:3847"  
/clone="GENOME SYSTEMS CLONE ID: Gm-cl068-3120"  
/tissue\_type="leaf, drought stressed, 1 month old plants, greenhouse grown"  
/lab\_host="DH10B"  
/clone\_lib="Gm-cl068"  
/note="Vector: pBluescript II SK+; Site 1: EcoRI; Site 2: XhoI; The cDNA library was constructed from mRNA isolated from drought stressed leaf tissue of the cultivar Williams 82. The month old greenhouse grown plants were deprived of water for 3 days prior to harvesting the stressed leaf tissue. Complementary DNA was synthesized from mRNA using a primer consisting of a poly(dT) sequence with a XhoI restriction site. EcoRI adapters were ligated to the blunt-ended cDNA fragments followed by XhoI digestion. The blunt-ended cDNA fragments followed by XhoI digestion. The EcoRI-XhoI restriction site of the pBluescript vector. The ligated cDNA fragments were transformed into DH10B host cells (GibcoBRL). This library was constructed in the laboratory of Dr. Randy Shoemaker."

BASE COUNT 152 a 120 C 112 G 181 t  
RIGIN  
Query Match 40.2%; Score 101; DB 12; Length 565;  
Best Local Similarity 100.0%; Pred. No. 3e-42;  
Matches 101; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
125 TTCCAAACCATGTCACAGTCATCTAAGTTTCGCCCTTTGGGATTCTAGGTAACATTGC 184  
|||||  
100 TTCCAAACCATGTCACAGTCATCTAAGTTTCGCCCTTTGGGATTCTAGGTAACATTGC 159  
|||||  
185 CTCCTTCGTGTGCTTTCTGGCACCACCTACCAACATTTTATA 225  
|||||  
160 CTCCTTCGTGTGCTTTCTGGCACCACCTACCAACATTTTATA 200  
|||||

RESULT 14  
BU090543 458 bp mRNA linear EST 29-AUG-2002  
LOCUS su06b06.y1 Gm-cl066 Glycine max cDNA clone GENOME SYSTEMS CLONE ID:  
DEFINITION Gm-cl066-827 5' similar to TR:082587 082587 MTN3 HOMOLOG. ;, mRNA sequence.  
ACCESSION BU090543  
VERSION BU090543.1 GI:22540700  
KEYWORDS EST.  
SOURCE Glycine max (soybean)  
ORGANISM Glycine max  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids

; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.  
REFERENCE 1 (bases 1 to 458)  
AUTHORS Shoemaker,R., Keim,P., Vodkin,L., Erpelding,J., Coryell,V., Khanna ,A., Bolla,B., Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers ,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk ,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann ,R., Waterston,R. and Wilson,R.  
TITLE Public Soybean EST Project  
JOURNAL Unpublished  
COMMENT Contact: Shoemaker R/Public Soybean EST Project  
Public Soybean EST Project  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: est@watson.wustl.edu  
This clone is available through: Genome Systems, Inc. 4633 World Parkway Circle St. Louis, Missouri 63134 For further information call: (800) 430-0030 or (314) 427-3222 FAX:(888) 919-3324 or (314) 427-3324 or contact: clones@genomesystems.com or info@genomesystems.com web site: www.genomesystems.com  
High quality sequence stop: 421.  
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/note="Vector: pBluescript II SK+; Site 1: EcoRI; Site 2: XhoI; The cDNA library was constructed from mRNA isolated from unexpanded leaves and the shoot tips of 2 week old seedling from the cultivar Williams. The 2 week old seedlings were salt stressed in a solution of 500mM NaCl for 3 days prior to harvesting. Complementary DNA was synthesized from mRNA using a primer consisting of a poly(dT) sequence with a XhoI restriction site. EcoRI adapters were ligated to the blunt-ended cDNA fragments followed by XhoI digestion. The cDNA fragments were directionally cloned into the EcoRI-XhoI restriction site of the pBluescript vector. The ligated cDNA fragments were transformed into DH10B host cells (GibcoBRL). This library was constructed in the laboratory of Dr. Randy Shoemaker."

BASE COUNT 122 a 97 C 93 G 144 t 2 others  
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Db 2 GTTGTGTGACACAGAAATTAAGCTAGAGCTTCATAGTTTCTTCTTTTCTCACCTTCC 61  
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|||||  
Db 62 TTCTCTCCCTTCAGACAAAGGGACAAAATC 93  
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VERSION BM085196.1 GI:16995824

**EYWORDS**  
**SOURCE**  
**ORGANISM**  
 EST.  
 Glycine max (soybean)  
 Glycine max  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids  
 ; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;  
 Glycine.  
**REFERENCE**  
 1 (bases 1 to 564)  
**AUTHORS**  
 Shoemaker, R., Keim, P., Vodkin, L., Erpelding, J., Corvett, V., Khanna  
 , A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C.,  
 Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers  
 , Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk  
 , R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann.  
 , R., Waterston, R. and Wilson, R.  
**TITLE**  
 Public Soybean EST Project  
**JOURNAL**  
 Unpublished  
**COMMENT**  
 Contact: Shoemaker R/Public Soybean EST Project  
 Public Soybean EST Project  
 Washington University School of Medicine  
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA  
 Tel: 314 286 1800  
 Fax: 314 286 1810  
 Email: est@watson.wustl.edu  
 This clone is available through: ResGen, Invitrogen Corp. 2130  
 South Memorial Parkway Huntsville, AL 35801 For further information  
 call: (800)-533-4363 or contact: ccu@resgen.com web site:  
 www.resgen.com

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FEATURES
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Location/Qualifiers
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old seedling"
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XhoI; The cDNA library was constructed from mRNA isolated
from unexpanded leaves and the shoot tips of 2 week old
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seedlings were salt stressed in a solution of 500mM NaCl
for 3 days prior to harvesting. Complementary DNA was
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transformed into DH10B host cells (GibcoBRL). This library
was constructed in the laboratory of Dr. Randy

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BASE COUNT		ORIGIN	
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